

FIG. 1

ATGGCGCCGCGCCGCGCCGCGCGCTGCTGCCCCGTGCTGCTGCTCCTGGCCGCGCCGCGCCGCGCCCTGCCGGCGATGGGGCTGCG  
 AGCGGCGCGCTGGGAGCCGCGGTACCCGGCGGGACCCGCGCCCTTCGCCCTCCGGCCCGGCTGTACCTACGCGGTGGGCG  
 CCGCTTGACAGCCCCCGGCGCCCGCGGGAGCTGCTGGACGTGGGCGCGGATGGGCGGCTGGCAGGACGTCGGCGCGCTCTCG  
 GCGCGCGGGCGCCCGCTGCCGCTGCAAGTCCGCTTGGTGCCCGCAGTGCCCCGACGGCGCTGAGCCGCGCCCTGCGGGC  
 GCGCACGCACCTTCCCGGCTGCGGAGCCCGTGCCCGGCTCTGCGGAACCGGTGCCCGGCTCTGCGGGGCGCTCTGCTTCC  
 CCGTCCCCGGCGGCTGCGCGCGCGCGCAGCATTGCGCGCTCGCAGCTCCGACCACCTTACCCGCTGCCGCTGCCCGCGC  
 CGCCCCAGGCCCCGCTGTCCCGGCGCTCCCATCTGCTGCCCGCGGGCGGCTCGGTCCGCTGCGTCTGCTGTGCGCCCT  
 GCGGCGCGCGGCTGGCGCCGTCCGGGTGGGACTGGCGCTGGAGGCCGCCACCCCGGGGACGCCCTCCGCTGCGCATCCC  
 CATCGCCGCCCCCTGCCGCGCAACTTGCCCCGAAGCCCGGGCGGGGCGCGCGACGGGCCCGGCGGGGCGACGAGCGGCGAGA  
 GGGAGCCTGAAGTTTCCGATGCCCAACTACAGGTGGCGTTGTTTGAGAACGAACCGGCGGGGACCCCTCATCTCCAGCT  
 GCACCGCGACTACACCATCGAGGGCGAGGAGGAGCGCGTGAGCTATTACATGGAGGGGCTGTTCGACGAGCGCTCCCGGG  
 GCTACTTCCGAATCGACTCTGCCACGGGCGCGGTGAGCACGGACAGCGTACTGGACCGCGAGACCAAGGAGACGCACGTC  
 CTCAGGGTGAAAGCCGTGGACTACAGTACGCGCGCGCGCTCGGCCACACCTACATCACTGTCTTGGTCAAAGACACCAA  
 CGACCACAGCCCGGTCTTCGAGCAGTCGGAGTACCGCGAGCGGTGCGGGAGAACCTGGAGGTGGGCTACGAGGTGCTGA  
 CCATCCGCGCCAGCGACCCGACTCGCCCCATCAACGCCAACTTGCGTTACCCGCTGTTGGGGGGCGCGTGGGACGTCTTC  
 CAGCTCAACGAGAGCTCTGGCGTGGTGAGCACACGGGCGGTGCTGGACCGGGAGGAGGCGGCGGAGTACCAGCTCCTGGT  
 GGAGGCCAACGACCAGGGGCGCAATCCGGGCGCGCTCAGTGCCACGGCCACCGTGTACATCGAGGTGGAGGACGAGAACG  
 ACAACTACCCCACTTCAGCGAGCAGAACTACGTGGTCCAGGTGCCCGAGGACGTGGGGCTCAACACGGCTGTGCTGCGA  
 GTGCAGGGCCACGGACCGGGACCGGGCCAGACGCGGCCATTCACTACAGCATCCTCAGCGGGAACGTGGCCGCGCAATT  
 CTACCTGCACTCGCTGAGCGGGATCCTGGATGTGATCAACCCCTTGGATTTCGAGGATGTCCAGAAATACTCGCTGAGCA  
 TTAAGGCCCAGGATGGGGGCGGCCCCCGCTCATCAATTCTTCAGGGGTGGTGTCTGTGCAGGTGCTGGATGTCAACGAG  
 AACGAGCCTATCTTTGTGAGCAGCCCTTCCAGGCCACGGTGTGCGAGAATGTGCCCTGGGCTACCCCTGGTGCACAT  
 TCAGGCGGTGGACGCGGACTCTGGAGAGAACGCCCGGCTGCACTATCGCCTGGTGGACACGGCTCCACCTTCTGGGGG  
 GCGGCAGCGCTGGGCCCTAAGAATCTGCCCCACCCCTGACTTCCCCTTCCAGATCCACAACAGCTCCGGTTGGATCACA  
 GTGTGTGCCGAGCTGGACCGCGAGGAGGTGGAGCACTACAGCTTCGGGGTGGAGGCGGTGGACCACGGCTCGCCCCCAT  
 GAGCTCCTCCACCAGCGTGTCCATCACGGTGCTGGACGTGAATGACAACGACCCGGTGTTCACGCAGCCACCTACGAGC  
 TTCGTCGAAATGAGGATGCGGCGCGTGGGGAGCAGCGTGCTGACCTGCAGGCCCCCGACCGTGACGCCAACAGTGTGATT  
 ACCTACCAGCTCACAGGCGGCAACACCCGGAACCGCTTTGCACTCAGCAGCCAGAGAGGGGGCGGCTCATCACCCCTGGC  
 GCTACCTCTGGACTACAAGCAGGAGCAGCAGTACGTGCTGGCGGTGACAGCATCCGACGGCACACGGTCCGACACTGCGC  
 ATGTCTAATCAACGTCACTGATGCCAACACCCACAGGCGCTGCTTTTCAGAGCTCCATTACACAGTGAGTGTCAGTGAG  
 GACAGGCGCTGTGGGGACCTCCATTGCTACCTCAGTGCCAACGATGAGGACACAGGAGAGAATGCCCGCATCACCTACGT  
 GATTCAGGACCCCGTGCCGCGAGTTCCGCATTGACCCCGACAGTGCCACCATGTACACCATGATGGAGCTGGACTATGAGA

DATE	DESCRIPTION	AMOUNT	BALANCE
1890	Jan 1		100.00
	Feb 1	50.00	50.00
	Mar 1	25.00	25.00
	Apr 1	10.00	15.00
	May 1	75.00	90.00
	Jun 1	30.00	60.00
	Jul 1	15.00	45.00
	Aug 1	20.00	25.00
	Sep 1	10.00	15.00
	Oct 1	5.00	10.00
	Nov 1	12.00	22.00
	Dec 1	8.00	14.00
1891	Jan 1	18.00	32.00
	Feb 1	22.00	10.00
	Mar 1	15.00	5.00
	Apr 1	10.00	15.00
	May 1	20.00	35.00
	Jun 1	12.00	23.00
	Jul 1	8.00	15.00
	Aug 1	15.00	30.00
	Sep 1	10.00	20.00
	Oct 1	5.00	15.00
	Nov 1	12.00	27.00
	Dec 1	8.00	19.00
1892	Jan 1	18.00	37.00
	Feb 1	22.00	15.00
	Mar 1	15.00	0.00
	Apr 1	10.00	10.00
	May 1	20.00	30.00
	Jun 1	12.00	18.00
	Jul 1	8.00	10.00
	Aug 1	15.00	25.00
	Sep 1	10.00	15.00
	Oct 1	5.00	10.00
	Nov 1	12.00	22.00
	Dec 1	8.00	14.00

ACGAGGTCGCTACACGCTGACCATCATGCGCCAGGACAAACGGCATCCCGCAGAAATCAGACACACCCACCTAGCATC  
CTCATCCTCGATGCCAATGACAATGCACCCAGTTCCCTGTGGGATTTCTACACAGGGTTCCATCTTTGAGGATGCTCCAC  
CTCGACACGATCCTCCAGGTCTCTGCCACGGACCGGACTCAGGTCCCAATGGGCGTCTGCTGTACACCTTCCAGGGTG  
GGGACGACGGCGATGGGGACTTCTACATCGAGCCACGTCCGGTGTGATTTCGACCCAGCCCGGCTGGACCGGGAGAAT  
GTGGCCGTGTACAACCTTTGGGCTCTGGCTGTGGATCGGGGACGTCCCACTCCCTTAGCGCTCGGTAGAAATCCAGGT  
GACCATCTTGGACATTAATGACAATGCCCCATGTTTGGAGAAGGACGAACTGGAGCTGTTTGTGAGGAGAACAACCCAG  
TGGGGTCTGGTGGTGGCAAAGATTCTGTGCTAACGACCCGTGATGAAGGCCCTAATGCCAGATCATGTATCAGATTGTGGAA  
GGGGACATGCGGCATTTCTTCCAGCTGGACCTGCTCAACGGGACCTGCGTGGCATGGTGGAGCTGGACTTTGAGGTCCG  
GCGGAGTATGTGCTGGTGGTGACGGCCACGTGCGCTCCGCTGGTGGAGCCGAGCCACGGTGACATCCTTCTCGTGGACC  
AGAATGACAACCCGCTGTGCTGCCCCGACTTCCAGATCCTCTTCAACAACATATGTACCAACAAGTCCAACAGTTTCCCG  
ACCGGCTGTATCGGCTGCATCCCGGCCCATGACCCCGACGTGTGACACAGCCTCAACTACACCTTCTGTGACGGGCAACGA  
GCTGCGCTGTGTGTGCTGCTGACCCCGGCAACTGACAGCTCAGCCGCGACCTGGACAACAACCGGCCGCTGGAGG  
CGCTCATGTGAGGTGTCTGTGTCTGATGGCATCCACAGCTCAGCGCCTTCTGACCTTCCGCTGGTGCATCATCACGGAC  
GACATGCTGACCAACAGCATCACTGTGCGCTGGAGAAGATGTCCAGGAGATTTCTGTCCCGCTGTGTGGCCCTCT  
CGTGGAGGGGGTGGCCGCGCTGCTGTCCACCACCAAGGACGACGTCTTCTGCTTCAACGTCAGAACGACACCGACGTCA  
GCTCCAACATCCTGAACGTGACCTTCTCGGCGCTGTGCTTGGCGGCGTCCGCGGCCAGTTCTTCCCGTGGAGGACCTG  
CAGGAGCAGATCTACCTGAATCGAGCGCTGCTGACCACCATCTCCACGACGCGCTGTGCTGCCCTTCGACGACAACATCTG  
CCTGCGGAGGCCCTGCGAGAACTACATGAAGTGGTGTCCGTTCTGCGATTGACAGCTCCGCGGCCCTTCTCAGCTCCA  
CCACCGTGTCTTCCCGGCCATCCACCCCATCAACGGCTGCGCTGCGCTGCCGCGCCGCTTACCGGCGACTACTGC  
GAGACGGAGATCGACCTCTGCTACTCCGACCCGTGCGGCCCAACGGCCGCTGCCGCGAGCCGCGAGGGCGCTACACCTG  
CGAGTGTCTCGAGGACTTCACTGGAGAGCACTGTGAGGTGGATGCCCCGCTCAGGCGCGCTGTGCCAACGGGGTGTGCAAGA  
ACGGGGGACACTGCGTGAACCTGCTCATCGGCGCTTCCACTGCGTGTGTCTCTTGGCGAGTATGAGAGGGCCCTACTGT  
GAGGTGACCAACCGAGGCTTCCCGCCCATGCTTCTGCTACCTTCCGGGCGCTGAGACAGCGCTTCCACTTACCATCTC  
CCTCAGCTTTGCCACTCAGGAAGAAGCAAGCTTGTCTTCTACAAACGGCGCTTCAATGAGAAGCAGCACTTCATCGCCC  
TGGAGATCGTGGACGAGCAGGTGACAGCTACCTTCTCTGAGCGGAGACAACAACCGTGGCAGCCAGAGTTCCCACT  
GGTGTGAGTGACGGGCGGTGGCACTCTGTGCAAGTGCAGTACTACAACAAGCCCAATATTGGCCACCTGGGCGTGGCCCA  
TGGGCGCTCCGGGGAAAAGATGGCCGTGGTGCAGTGGATGATTGTGACACAACCATGGCTGTGCGCTTTGGAAGGACA  
TCGGGAACCTACAGCTGCGCTGCCAGGGGACTCAGACCGGCTCCAAGAAGTCCCTGGATCTGACCGGCCCTCTACTCCTG  
GGGGGTGTCCCAACCTGCCAGAAGACTTCCAGTGACAAACGGGAGTTCTGTGGGTGCATGCGGAACCTGTGAGTGA  
CGGCAAAAATGTGGACATGGCCGATTTCATCGCCAACAATGGCAACCGGGAGGCTGCGCTGCTCGGAGGAACCTTCTGCG  
ATGGGAGGCGGTGTGAGAATGGAGGCACCTGTGTCAACAGGTGGAATATGTATCTGTGTGAGTGTCCACTCCGATTCCGC  
GGGAAGAACTGTGAGCAAGCCATGCTCACCCTCAGCTCTTTCAGCGGTGAGAGCGTCTGTGCTTGGAGTGACCTGAACAT  
CATCATCTCTGTGCCCTGGTACCTTGGGGCTCATGTTCCGACCCCGGAAGGAGGACAGCGTTCTGATGGAGGGCCACCAGTG  
GTGGCCCCACGAGCTTTCGGCTCCAGATCTGACAACTACCTCCAGTTTTCAGGTGTCCACGGCCCCCTCCGATGTGGAG  
TCCGTGATGCTGTCCGGGTGCGGGGTGACCGACGGGAGTGGCAACCTGCTGTGATCGAGCTGAAGAATGTTAAGGAGGA  
CAGTGAGATGAAGCACCTGCTCACCATGACCTTGGACTATGGGATGGACGAGCAAGGAGATATCGGGGCGATGCTTC  
CCGGGCTGACGCTAAGGAGCGTGGTGGTGGAGGCGCTCTGAAGACAAGGTCTCCGCTGCGCCGTGGATTCCGAGGCTGC  
ATGCAAGGAGTGGAGTGGGGGGGACGCCACCAACGTGCGCACCTGAACATGAACAACGCACTCAAGGTGAGGGTGAA  
GGACGGCTGTGATGTGGACGACCCCTGTACCTCGAGCCCTGTCCCCCAATAGCCGCTGCCACGACGCTTGGAGGACT  
ACAGCTGCGTCTGTGACAAAGGGTACCTTGGAAATAACTGTGTGGATGCCGTGTACCTGAACCCCTGCCAGAACATGGGG  
GCCTGCGTGGCTCCCCCGGCTCCCCGACGGGCTACGTGTGCGAGTGTGGGCCCAAGTCACTACGGGCGCTACTGTGAGAA  
CAAACCTGACCTTCCGTGCCCCAGAGGCTGGTGGGGGAACCCCGCTCTGTGGACCCCTGCCACTGTGCCGTGACCAAGGCT  
TTGATCCCGCATGTAAATAAGACCAACGGCCAGTGCCAATGCAAGGAGAATTACTACAAGCTCCTAGCCCAGGACACCTGT  
TCTGCCCTGCGACTGCTTCCCCCATGGCTCCCCACCGGCACTTGGCAGATGGCCACCGGGCAGTGTGCTGCAAGCCCGG  
CGTCATCGGGCGGCAAGTGTGCAACCGCTGCGACAAACCGCTTGGCGAGGTACCAACGCTCGGCTGTGAAGTGATCTACAATG  
GCTGTCCCAAAGCATTTGAGGCGGGCATCTGTGTGGCCACAGACCAAGTTCGGCAGCGCGCTGCGGTGCCATGTCCCTAAG  
GGATCCGTGGAAATGCGGTCCGACACTGCAGCGGGGAGAAGGGCTGGCTGCCCCAGAGCTCTTTAACTGTACCCACCAT  
CTCCTTCTGTGACCTCAGGGCCATGAATGAGAAGCTGAGCCGCAATGAGACGAGGTGGACGGGCGCAAGGCGCTGACG  
TGGTGGAGGGCGCTCCGCAAGTGTACACAGCACACGGGACGCTCTTTGGCAATGAGTGGCGACGGCTTACCAAGCTGTG  
GGCCACGTCCTTCAGCACGAGAGCTGGCAGCAGGGCTTCGACCTGGCAGCCACGAGGACGCGACTTTCAGGAGGACGT  
CATCCACTCGGGCAGCGCCCTCTTGGCCCCAGCCACCAGGGCGCGCTGGGAGCAGATCCAGCGGAGCGAGGGCGGCACGG  
CACAGCTGCTCCGGCGCTCGAGGGCTACTTCAGCAACGTGGCACCAACGTGCGGCGGACGTACCTGCGGCGCTTCTGTC  
ATCGTACCGCCAAACATGATTCTTGTGTGACATCTTTGACAAAGTTCAAACCTTACGGGAGCCAGGGTCCCCGCGATTGCA  
CACCATCCATGAAGAGTTCCCGAGGAGACTGGAGTCTCCGCTCTCCTTCCAGCCGACTTCTTCAGACCACTGAAGAAA  
AAGAAGGCCCCCTGCTGAGGCGGGCTGCGCGAGGACCAACCCGAGCAACGCGCCCGGGGCTGGCACCGAGAGGGAG  
GCCCCGATCAGCAGGCGGAGGCGACACCTGATGACGCTGGCCAGTTCCGCGCTGCTTGTGATCATATTACGACCCCT  
GGGGCAGCTCCTGCGCGAGGCTACGACCCCGACCGCTCGCAGCTTCCGGTTGGCTTACCGGCCCATTAATACCCCGA  
TGGTGACACGCTGCTGTACAGCGAGGGGCTCCGCTCCCGAGACCCCTGGAGAGGGCGCTGCTGGTGGAGTTCCGCCGTG  
CTGGAGGTGGAGGAGCGAACCAAGCTGTCTGCTGTCTTGGAAACCTCCTTGGCCGTGGTGGGACGGGAGGGTGGT

FIG. 1 Continued

TGCCCCGGGGCTGCGAGCTCCTGTCCAGGAACCGGACACATGTCCCTGCCAGTGCAGCCACACAGCCAGCTTTGCGGTGC  
TCATGGATATCTCCAGGCGTGAGAACGGGGAGGTCCCTGCCTCTGAAGATTGTACCTATGCCGCTGTGTCTTTGTCACCTG  
GCAGCCCTGCTGGTGGCCPTTCGTCCCTCCCTGAGCCTGGTCCGCATGCTGCGCTCCAACCTGCACAGCATTACAAAGCACCT  
CGCCGTGGCGCTCTTCTCTCTCAGCTGGTGTTCGTGATTGGGATCAACCAGACGGAAAACCCGTTTCTGTGCACAGTGG  
TTGCCATCTCTCCACTACATCTACATGAGCACCTTTGCCTGGACCTTCGTGGAGACCTGCATGTCTACCGCATGCTG  
ACCGAGGTGCGCAACATCGACACGGGGCCCATGCGGTTCTACTACGTGCTGGGCTGGGGCATCCCGGCCATTGTCACAGG  
ACTGGCGGGTCGGCCTGGACCCCCAGGGCTACGGGAACCCCGACTTCTGCTGGCTGTGCTTTCAAGACACCCCTGATTTGGA  
GCTTTGCGGGGGCCCATCGGAGCTGTTATAATCATCAACACAGTCACTTCTGTCTATCTGCAAAGGTTTCTGCCAAAGA  
AAGCACCATATTATGGGAAAAAAGGGATCGTCTCCCTGCTGAGGACCGCATTCCTCTGCTGCTGCTCATCAGCGCCAC  
CTGGCTGCTGGGGCTGCTGGCTGTGAACCGCGATGCACTGAGCTTTCACTACCTCTTCGCCATCTTCAGCGGCTTACAGG  
GCCCTTCTGCTCCTCTTTTCCACTGCGTGTCAACCAGGAGGTCCGGAAGCACCTGAAGGGCGTCTCGGCGGGAGGAAG  
CTGCACCTGAGGAGTCCGCCACCACCAGGGCCACCCTGCTGACGCGCTCCCTCAACTGCAACACCCACTTCGGTGACGG  
GCCTGACATGCTGCGCACAGACTTGGGCGAGTCCACCGCTCGCTGGACAGCATCGTCAGGGATGAAGGGATCCAGAAGC  
TCGGCGTGTCTCTGGGCTGGTGAGGGGCAGCCACGGAGAGCCAGACGCGTCCCTCATGCCCAGGAGCTGCAAGGATCCC  
CCTGGCCACGATTCCGACTCAGATAGCGAGCTGTCCCTGGATGAGCAGAGCAGCTCTTACGCCCTCCTCACACTCGTCAAG  
CAGCCAGGACGATGGGGTGGGAGCTGAGGAAAAATGGGACCCGGCCAGGGGGCGCCCTCCACAGCACCCCCAAAGGGGACG  
CTGTGGCCAACCCACGTTCCGGCCGGCTGGCCCGAACCAGAGCCTGGCTGAGAGTGACAGTGAGGACCCAGCGGCAAGCCC  
CGCTTGAAGGTGGAGACCAAGGTCAGCGTGGAGCTGCACCGCGAGGAGCAGGGCAGTCACCGTGGAGAGTACCCCCCGGA  
CCAGGAGAGCGGGGGCGCAGCCAGGCTTGCTAGCAGCCAGCCCCAGAGCAGAGGAAAGGCATCTTGAAAAATAAAGTCA  
CCTACCCCGCCCGCTGACGCTGACGGAGCAGACGCTGAAGGGCCGGCTCCGGGAGAAGCTGGCCGACTGTGAGCAGAGC  
CCCACATCTCGCCGACGTCTTCCCTGGGCTCTGGCGGCCCCGACTGCGCCATCACAGTCAAGAGCCCTGGGAGGGAGCC  
GGGGCGTGACCACCTCAACGGGGTGGCCATGAATGTGCGCACTGGGAGCCCCAGCCGATGGCTCCGACTCTGAGAAAC  
CGTGA

FIG. 2

MAPPPPPVLPVLLLLAAAAALPAMGLRAAAWEPRVPGGTRAFALRPCTYAVGAACTPRAPRELLDVGRDGRLAGRRRVRS  
 GAGRPLPLQVRLVARSAPTALSRRRLRARTHLPGCGARARLCGTGARLCCGALCFPVPGGCAAAQHSALAAPTTLACRCPP  
 RPRPRCPGRPICLPFGGSVRLRLCALRAAGAVRVGLALEAATAGTFSASPSPPPLPPNLPEARAGPARRARRRGTSGR  
 GSKFPMPNYQVALFENEPAATLILQLHAHYTIEGEEERVSYMEGLFEDERSRGYFRIDSATGAVSTDSVLDRETKETHV  
 LRVKAVDYSTPPRSATTYITVLVKDINDHSPVFEQSEYRERVRENLEVGYEVLTIIRASDRDSPINANLRYRVLGGAWDF  
 QLNESSCVVSTRAVLDRREEAAYQLLVEANDQGRNPGLSATATVYIEVEDENDNYPQFSEQNYVVOVPEDVGLNTAVLR  
 VQATDRDQGGNAAIHYSILSGNVAGQFYLHSLSGILDVINPLDFEDVQKYSLSIKAQDGRPPLINSSGVVSVQVLDVND  
 NEPIFVSSPFQATVLENVPLGYPVVHIQAVDADSGENARLHYRLVDTASTFLGGGSAGPKNPAPTDFPFQIHNSSGWIT  
 VCAELDREEVEHYSFGVEAVDHGSPFMSSTSVSITVLDVNDNDEVFTQPTYELRLNEDAAGSSVLTILQARDRDANSVI  
 TYQLTGNTNRNRFALSSQRCGGLITLALPLDYKQEQQYVLAFTASDGTSTRHTAHVLINVTIDANTHRFPVQSSHYTVSVSE  
 DRPVGTSIATLSANDEDTGENARITYVIQDPVPQFRIDPDSGTMYTMMELDYENQVAYTLTITMAQDNGIPQKSDTTTLEI  
 LILDANDNAPQLWDFYQGSIFEDAPPBTSILQVSATDRDSCPNORLLYTFQGGDDGDCDFYIEPTSGVIRTRRLDREN  
 VAVYNLWALAVDRGSPTPLSASVEIQVTILDINDNAPMFEKDELELFEENNPFVGSVAKIRANDPEGENAQIMYQIVE  
 GDMRHFFQLDLLNGDLRAMVELDFEVRREYVLVVQATSAPLVSRATVHILLVDQNDNPFVLPDFQILFNNYVTNKSNSFP  
 TGVIIGCI PAHD PDVSDSLNYTFFVQGNELRLLLLD PATGELQLSRDLDMNRPLEALMEVSVSDGIHSVTAFCTLRVTIITD  
 DMLTNSITVRLENMSQEKFLSPLLALFVEGVA AVLSTTKDDVFVFNQNDTDVSSNINLVTF SALLPGGVRGQFFPSEDL  
 QEQIYLNRLTLLTTISTQRVLPFDNCLREPCENYMKCVSVLRFDSAPFLSSTTVLFRPIHPINGLRRCRCPFGFTGDCY  
 ETEIDL CYSDPCGANGRCRSREGGYTCECFEDFTGEHCEVDARSGRCA NGVCKNGGTCVNLLIGGFHCVCPPGEYERPYC  
 EVTTRSPFPQSVFTRGLRQRFGHTISLTFATQERNGLLYNGRNFNEKHDFIALEIVDEQVQLTF SAGETTTTVAPKVPS  
 GVS DGRWHSVQVOYNNKPNIGHLGLPHGPGSEKMAVTVDDCDTMAVRFKGKDIGNYSCAAQQTQTSKKSLLDTG PLLL  
 GGVPNL PEDF PVHNRQFVGC MRNLSVDGKNVDMAGFIANNGTREGCAARRNFC DGRRCONGGTCVNRWNMYLCECPLRF  
 GKNC EQAMPHPQLFSGESVVSWSDLNIIISVPWYLG LMFTRKEDSVLMEATSGGPTSFRLLQILNNYLQFEVSHGPSDVE  
 SVMLSGLRVTDGEWHLLIELKNVKEDSEM KHLVTMTLDYCMDQNKADIGGMLPGLTVRSVVVGASEDKVSVRRGFRGC  
 MQGVRMGCTPTNVATLNMNNA LKVRVKDGCDDVDPCTSSPCPPNSRCHDAWEDYSCVCDKGYLG INCV DACHLNPCENMG  
 ACVRSPGSPQGYVCEGFSHYGPYCENKLDLPCPRGWGNPVC GPCHCAVSKGFPDPCNKTNQCCQCKENYKLLAQDTC  
 LPCDCFPHGSHSRCTCDMATGQCACKPGVIGRQCNRCDNPF AEVTTLGCEVTYNGCPKAFEAGIWWPQTKFGQPAAVPCPK  
 GSVGNVVRHCSGEGKWLPELFNCTTISFVDLRAMNEKLSRNETQVDGARALQLVRALRSATQHTGT LFGNDVVRTAYQLL  
 GHVLQHESWQQGFDLAATQDADFHEVDI HSGSALLAPATRAAWEQIQRSEGCTAQLLRLECYFSNVARNVRRTYLRPFV  
 IVTANMILAVDIFDKFNFTGARVPRFDTHIEEFPRELESSVSFPADFFRPPEEKEG PLLRPAGRRTTPQTTRPGPGTERE  
 APISRRRRHPDDAGQFAVALVIIYRTLQQLLPERYDPRRSLRLPHRPIINTPMVSTLVYSECAPLPRPLERFVLVEFAL  
 LEVEERTKPVCFWNHSLAVGGTGGWSARGCELLSRNRTHVACQCSHTASEAVLMDISRRENGEVLPLKIVTYAAVSLSL  
 AALLVAFVLLSLVRMLRSNLHSIHKHLAVALFLSQLVFVIGINQ TENFFLCTVVAILLHYIYMSTFAWTLVESLHVYRML

TEVRNIDTGPMRFYYVVGWGI PAIVTGLAVGLDPQGYGNPDFCWL SLQDTLIWSFAGPIGAVIIINTVTSVLSAKVSCQR  
 KHHYYGKKGIVSLLRTAF LLLLLISATWLLGLLAVNRDALSFHYLFAIFSGLQGFVLLFHCVLNQEVRKHLKGVLGGRK  
 LHLED SATTRATLLTRSLNCTTFG DGPMLRTDLGESTASLDSIVRDEGIQKLG VSSGLVRGSHGEPDASLMFRSCKDP  
 PQHDS DSDSELSD EQSSSYASSHSSD SEDDGVAEEKWD PARGAVHSTPKGDAVANHV PAGWPDQSLAESDSEDPSGKP  
 RLKVETKVSVELHREBQGS HRGEYPPDQESGCAARLASSQPPEQRKGILKNKVITYPPPLTLTEQTLKGRLREKLADCEQS  
 PTSSRTSSLGSGGPDCAITVKS PCREPGRDHLNGVAMNVRTGSAQADGSDSEKP

FIG. 3

Score = 939 (140.9 bits), Expect = 4.0e-81, Sum P(3) = 4.0e-81  
Identities = 203/218 (93%), Positives = 203/218 (93%), Strand = Plus / Plus

Query: 230 CTGTAATAAGACCAACGGCCAGTGCCAAT-GCAAGGAGAATTACTACAAGCTCCTAGCCC 288  
CTG A T A A C GCC TG C T QCA GGAGAATTACTACAAGCTCCTAGCCC  
Sbjct: 38281 CTGAAGTCACAGGCCCTGCCTCTGGCTTTTGCA-GGAGAATTACTACAAGCTCCTAGCCC 38339

Query: 289 AGGACACCTGTCTGCCCTGCGACTGCTTCCCCCATGGCTCCCACAGCCGCACTTGCGACA 348  
AGGACACCTGTCTGCCCTGCGACTGCTTCCCCCATGGCTCCCACAGCCGCACTTGCGACA  
Sbjct: 38340 AGGACACCTGTCTGCCCTGCGACTGCTTCCCCCATGGCTCCCACAGCCGCACTTGCGACA 38399

Query: 349 TGGCCACCGGGCAGTGTGCCTGCAAGCCCGCGTCATCGGCCGCCAGTGCAACCGCTGCG 408  
TGGCCACCGGGCAGTGTGCCTGCAAGCCCGCGTCATCGGCCGCCAGTGCAACCGCTGCG  
Sbjct: 38400 TGGCCACCGGGCAGTGTGCCTGCAAGCCCGCGTCATCGGCCGCCAGTGCAACCGCTGCG 38459

Query: 409 ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG 447  
ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG  
Sbjct: 38460 ACAACCCGTTTGCCGAGGTCACCACGCTCGGCTGTGAAG 38498

FIG. 4

Score = 1000 (352.0 bits), Expect = 2.4e-98, P = 2.4e-98  
Identities = 162/186 (87%), Positives = 172/186 (92%), Frame = +3

Query: 3 YLGINCVDAHLNPCENMGACVRSPGSPQGYVCECGFSHYGPYCENKLDLPCPRGWWGNP 182  
Y G CVDAC LNPC+++ ACVRSP +P+GY CECGP HYG YCENK+DLPCP+GWWGNP  
Sbjct: 1917 YFGKKCVDACLLNPCKHVAACVRSPNTPRGYSCECGPGHYGYCENKVDLPCPKGWWGNP 1976

Query: 183 VCGPCHCAVSKGFDPDCNKTNQGQCCKENYYKLLAQDTCLPCDCFPHGSHSRCTCDMATGQ 362  
VCGPCHCAVS+GFDPDCNKTNQGQCCKENYYK AQD CLPCDCFPHGSHSR CDM TGQ  
Sbjct: 1977 VCGPCHCAVSQGFDPDCNKTNQGQCCKENYYKPPAQDACLPDCFPHGSHSRACDMDTGQ 2036

Query: 61 CCTGCGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGGGCCCCAGTCACT 120  
|||||  
Sbjct: 33445 CCTGCGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGGGCCCCAGTCACT 33504

Query: 121 ACGGGCCGTACTGTGAGAACAA 142  
|||||  
Sbjct: 33505 ACGGGCCGTACTGTGAGAACAA 33526

FIG. 5

Score = 12924 (4549.5 bits), Expect = 0.0, P = 0.0  
 Identities = 2451/3034 (80%), Positives = 2677/3034 (88%)

Query: 1 MAPPPFPVLPVLLLLAAAAALPAMGLRAAAWEPRVPGGTRAFALRPGCTYAVGAACTPR- 59  
 MAP P VLP L+LLAAAA LPA+ L AAWE RVPGG RAFAL PG +Y + TPR

Sbjct: 1 MAPSSPRVLPALVLLAAAA-LPALELGAAAWELRVPGGARAFALGPCWSYRLDTRTPRE 59

Query: 60 ---APRELLDVGRD-GRLAGRRRVSG-AGRPLPLQVRLVARSAFTALSRRRLRARTHLPGC 114  
 RE GR G AG + AGR LPLQVRLVAR APTA S LRAR + C

Sbjct: 60 LLDVSREGPAAGRRLGLGAGTLGCARLGRLLPLQVRLVARGAFTAPSLVLRARAYGARC 119

Query: 115 GARA-RLCGTGARL-----CG-ALCFVPGGCAAAQHSALAAPTTLPACRCPPRP 162  
 G R R GA L G ALCFP GG AA+ S L A T PAC CPP

Sbjct: 120 GVRLRRSARGAELRSPAVRSVPGLGDALCFPAAGGGAASLTSVLEAITNFPACSCPPVA 179

Query: 163 RPRCPGRPICLPFGGSVRLRLCALRRAGAVRVGLALEAATAGTPSASPSPPPLPPNL 222  
 C PICL PGGS LRL+CAL RAAGAV V L ++A T+GTPS SPS SP L NL

Sbjct: 180 GTGCRRGPICLRPGGSABLRLVLCALGRAAGAVVVELVIQA-TSGTPSESFSVSPSLL-NL 237

Query: 223 PEARAGPARRARRGTSGRGSLKFPMPNYQVALFENEPAGTLILQLHAHYTIEGEEERSVY 282  
 + RAG RR+RRGT S +FP+P+YQV++ ENEPAGT +++L AH EG+ R+SV

Sbjct: 238 SQPRAGVVRRSRRCTGSSTSPQFPLPSYQVSVPENEPAGTAVIELRAHDPDEGDAGRLSY 297

Query: 283 YMEGLFDESRGYFRIDSATGAVSTDSVLDRETKETHVLRVKAVDYSTPPRSATTYITVL 342  
 ME LFDERS GYF ID+ATGAV+T LDRETK+THVL+V AVD+ +P RSA TY+TV

Sbjct: 298 QMEALFDESRNGYFLIDAATGAVTTARSLDRETKDTHVLKVSVDHGSPPRRSAATYLTVT 357

Query: 343 VKDTNDHSPVFQSEYRERRENLEVGVEVLTIRASDRDSPINANLRYRVLGGAWDVFLQ 402  
 V DTNDHSPVFQSEYRER+RENLEVGVEVLTIRA+D D+P NAN+RYR+L GA VF++

Sbjct: 358 VSDTNDHSPVFQSEYRERIRENLEVGVEVLTIRATDGDAPSNANMRYRLLEGAGGVFEI 417

Query: 403 NESSGVVSTRAVLDRREEAAYQLLVEANDQGRNPGPLSATATVYIEVEDENDNYPQFSEQ 462  
 + SGVV TRAV+DREEAAYQLLVEANDQGRNPGPLSA+ATV+I VEDENDNYPQFSE+

Sbjct: 418 DARSGVVRTRAVVDREEAAYQLLVEANDQGRNPGPLSASATVHIVVEDENDNYPQFSEK 477

Query: 463 NYVVQVPEDVGLNTAVLRVQATDRDQGNAAIHYSILSGNVAGQFYLHSLSGILDVINPL 522  
 YVVQVPEDV +NTAVLRVQATDRDQGNAAIHYSI+SGN+ GQFYLHSLSG LDVINPL

Sbjct: 478 RYVVQVPEDVAVNTAVLRVQATDRDQGNAAIHYSIVSGNLKGQFYLHSLSGSLDVINPL 537

Query: 523 DFEDVQKYSLSIKAQDGGRPPLINSSGVSVQVLDVNDNEPIFVSSPFOATVLENVPLGY 582  
 DFE +++Y+L IKAQDGGRPPLINSSG+VSVQVLDVNDN PIFVSSPFOA VLENVPLG+

Sbjct: 538 DFEAIREYTLRIKAQDGGRPPLINSSGLVSVQVLDVNDNAPIFVSSPFOAAVLENVPLGH 597

Query: 583 PVVHIQAVDADSGENARLHYRLVDTASTFLGGGSAGPKNPAPTDFPFQIHNSSGWITVC 642  
 V+HIQAVDAD+GENARL YRLVDTAST +GG S +NPA PDPFQIHNSSGWITVC

Sbjct: 598 SVLHIQAVDADAGENARLQYRLVDTASTIVGGSSVDSENPAAPDFPFQIHNSSGWITVC 657

Query: 643 AELDREEVEHYSGVEAVDHGSPPMSSSTSVSITVLDVNDNDFVFTOPTYELRLNEDAAV 702  
 AELDREEVEHYSGVEAVDHGSP MSSS SVSITVLDVNDNDP+FTQP YELRLNEDAAV

Sbjct: 658 AELDREEVEHYSGVEAVDHGSPAMSSSASVSITVLDVNDNDPMFTQPVYELRLNEDAAV 717

Query: 703 GSSVLTLOARDRDANSVITYQLTGGNTRNRFALSSQGGGLITLALPLDYKQEQYVLAV 762  
 GSSVLT+L+ARDRDANSVITYQLTGGNTRNRFALSSQ GGGLITLALPLDYKQEQYVLAV

Sbjct: 718 GSSVLTLRARDRDANSVITYQLTGGNTRNRFALSSQSGGLITLALPLDYKQEQYVLAV 777

Query: 763 TASDGTRSHTAHVLINVTANTHRPVFQSSHYTVSVSEDRPVGTSIATLSANDEDTGENA 822  
 TASDGTRSHA V INVTANTHRPVFQSSHYTVSVSEDRPVGTSIAT+SA DEDTGENA

Sbjct: 778 TASDGTRSHAQVFINVTANTHRPVFQSSHYTVSVSEDRPVGTSIATISATDDEDTGENA 837

Query: 823 RITYVIQDPVPQFRIDPDSGTYMTMELDYENQVAYTLTMAQDNGIPQKSDTTTLEILI 882  
 RITYV++DPVPQFRIDP+GT+YTM ELDYE+Q AYTL I AQDNGIPQKSDTT+LEILI

Sbjct: 838 RITYVLEDVPVPQFRIDPDTGTIYTMELDYEDQAAYTLAITAQDNGIPQKSDTTTLEILI 897

# FIG. 5 Continued

Query: 883 LDANDNAPQFLWDFYQGSIFEDAPPSTSILOVSATDRDSGPNGRLLYTFQGGDDGDGDFY 942  
LDANDNAP+FL DFYQGS+FEDAPPSTS+LOVSATDRDSGPNGRLLYTFQGGDDGDGDFY

Sbjct: 898 LDANDNAPRFLRDFYQGSVFEDAPPSTSVLQVSATDRDSGPNGRLLYTFQGGDDGDGDFY 957

Query: 943 IEPTSGVIRTQRRLDRENVAVYNLWALAVDRGSP TPLSASVEIQVTILDINDNAPMFEKD 1002  
IEPTSGVIRTQRRLDRENVAVYNLWALAVDRGSP PLSASV IQV++LDINDN P+FEKD

Sbjct: 958 IEPTSGVIRTQRRLDRENVAVYNLWALAVDRGSPNPLSASVGIQVSULDINDNPPVFEKD 1017

Query: 1003 ELELFVEENNFPVGSVVAKIRANDPDEGPNQAIIMYQIVEGDMRHHFQLDLLNGDLRAMVEL 1062  
ELELFVEEN+PVGSVVA+IRANDPDEGPNQAI+YQIVEG++ FQDLL+GDLRA+VEL

Sbjct: 1018 ELELFVEENSPVGSVVARIRANDPDEGPNQAIYQIVEGNVPEVFQDLLSGDLRALVEL 1077

Query: 1063 DFEVRREYVLVQATSAPLVSRA TVHILLVDQNDNPPVLPDFQILFN NYVTNKSNSFPPTG 1122  
DFEVR+Y+LVVQATSAPLVSRA TVHI L+QNDNPP LPDFQILFN NYVTNKSNSFP+G

Sbjct: 1078 DFEVRDYMLVQATSAPLVSRA TVHIRLLDQNDNPPPELPDFQILFN NYVTNKSNSFP+G 1137

Query: 1123 VIGCIPAHDPDVS DLSNYTFVQGNELRLLLLD PATGELQLSRDL DNNRPLEALMEVSVSD 1182  
VIG IPAHDPD+SDLSNYTF+QGNEL LLLLD PATGELQLSRDL DNNRPLEALMEVSVSD

Sbjct: 1138 VIGRIPAHDPDLSDLSNYTFVQGNELSLLLLD PATGELQLSRDL DNNRPLEALMEVSVSD 1197

Query: 1183 GIHSVTAFCTLRVTIITDDMLTNSITVRLENMSQEKFLSP LLLALFVEGVAAVLSTTKDDV 1242  
GIHSVTA CTLRVTIITDDMLTNSITVRLENMSQEKFLSP LL+LFVEGVA VLSTTKDD+

Sbjct: 1198 GIHSVTALCTLRVTIITDDMLTNSITVRLENMSQEKFLSP LLSLFVEGVATVLSTTKDDI 1257

Query: 1243 FVFNQNDTDVSSN ILNVTF SALLPGGV RGQFPSED LQEQIYLNRTLLTTISTQ RVLPF 1302  
FVFN+QNDTDVSSN ILNVTF SALLPGG RG+FPSED LQEQIYLNRTLLTTIS QRVLPF

Sbjct: 1258 FVFNQNDTDVSSN ILNVTF SALLPGGTRGRFPSED LQEQIYLNRTLLTTISAQ RVLPF 1317

Query: 1303 DDNICLREPCENYMKCVSVLRFDSSAPFLSSTTVLFRPIHP INGLRCRCPPGFTGDYCET 1362  
DDNICLREPCENYMKCVSVLRFDSSAPF+SSTTVLFRPIHPI GLRCRCPPGFTGDYCET

Sbjct: 1318 DDNICLREPCENYMKCVSVLRFDSSAPFISSTTVLFRPIHPITGLRCRCPPGFTGDYCET 1377

Query: 1363 EIDL CYSDPCGANGRCRSREGGYTCECFEDFTGEHC EVDARSGRCA NGVCKNGGTCVNLL 1422  
EIDL CY+S+PCGANGRCRSREGGYTCECFEDFTGEHC+V+ RSGRCA+GVCKNGGTCVNLL

Sbjct: 1378 EIDL CYSNPCGANGRCRSREGGYTCECFEDFTGEHCQVNRSGRCASGVCKNGGTCVNLL 1437

Query: 1423 IGGFHCVCPPGEYERPYCEVTRSFPPQSFVTFRGLRQRFHFTISLTFATQERNGLLLYN 1482  
IGGFHCVCPPGEYE PYCEV+TRSFPPQSFVTFRGLRQRFHFT+SL FATQ+RN LLLYN

Sbjct: 1438 IGGFHCVCPPGEYEHYCEVSTRSFPPQSFVTFRGLRQRFHFTVSLAFATQDRNALLYN 1497

Query: 1483 GRFNEKHDFIALEIVDEQVQLTFSAGETTTTVAPKVP SGVSDGRWHSVQVQYYNKPNIGH 1542  
GRFNEKHDFIALEIV+EQ+QLTFSAGETTTTV P+VP GVSDGRWHSV VQYYNKPNIGH

Sbjct: 1498 GRFNEKHDFIALEIVBEQQLTFSAGETTTTVTPQVGGVSDGRWHSVLVQYYNKPNIGH 1557

Query: 1543 LGLPHGPSGCKMAVVTDDCDTMAVRFGKDIGNYSCAAQGTQTGSKKSLDLTG PLLLGG 1602  
LGLPHGPSGCK+AVVTDDCD +AV FG +GNYSCAAQGTQ+GSKKSLDLTG PLLLGG

Sbjct: 1558 LGLPHGPSGCKVAVVTDDCDAVAVHFGSVGNYSCAAQGTQSGSKKSLDLTG PLLLGG 1617

Query: 1603 VPNLPEDFP VHNRFVGC MRNLSVDGKNVDMAGFIANNGTREGCAARRNFC DGRRCQNGG 1662  
VPNLPEDFP VH+RFVGC MRNLS+DG+ VDMA FIANNGTREGCAARRNFC DGRRCQNGG

Sbjct: 1618 VPNLPEDFP VHSRQFVGC MRNLSIDGRIVDMAAFIANNGTREGCASQRNFC DGTSCQNGG 1677

Query: 1663 TCVNRWNMYLCECPLRFGGKNCEQAMPHPQLFSGESVVSWSDLNIIISVPWYLGLMFRTR 1722  
TCVNRWN YLCECPLRFGGKNCEQAMPHPQ F+GESVV WSDL+I ISVPWYLGLMFRTR

Sbjct: 1678 TCVNRWNTYLCECPLRFGGKNCEQAMPHPQRF TGESVVLWSDLDITISVPWYLGLMFRTR 1737



# FIG. 5 Continued

Query: 2563 VRNIDTGPMRFYVVGWGI PAIVTGLAVGLDPQGYGNPDFCWL SLQDTLIWSFAGFIGAV 2622  
VRNIDTGPMRFY+VVGWGI PAIVTGLAVGLDPQGYGNPDFCWL SLQDTLIWSFAGP+G V

Sbjct: 2578 VRNIDTGPMRFYHVVGWGI PAIVTGLAVGLDPQGYGNPDFCWL SLQDTLIWSFAGPVGTV 2637

Query: 2623 IIINTVTSVLSAKVSCQRKHHYVGKKGIVSLRLTAFLLLLLLISATWLLGLLAVNRDALSF 2682  
IIINTV VLSAKVSCQRKHHY +KG+VS+LRTAFLLLLLL++ATWLLGLLAVN D LSF

Sbjct: 2638 IIINTVIFVLSAKVSCQRKHHYERKGVVSMRLTAFLLLLLLVATWLLGLLAVNSDTLSF 2697

Query: 2683 HYLFAIFSGLQGPVLLFHCVLNOEVRKHLKGVLCGRKLHLED SATTRATLLTRSLNCNT 2742  
HYLFA FS LQG FVLLFHCV ++EVRKHL+ VL G+KL L+DSATTRATLLTRSLNCN

Sbjct: 2698 HYLFAAFSCLQGI FVLLFHCVAHREVRKHLRAVLAKKQLQDLSATTRATLLTRSLNCNN 2757

Query: 2743 TFGDGPDMRLRTDLGESTASLDSIVRDEGIQKLGVS SGLVRGSHGEPDASLMPRSCKDPPG 2802  
T+ +GPDMLRT LGESTASLDS RDEG+QKL VSSG RG+HGEPD S +PR+ K G

Sbjct: 2758 TYSEGPDMLRTALGESTASLDSSTRDEGVQKLSVSSGPARGNHGEPDTSFIPRNSKKAHG 2817

Query: 2803 HDSDSDSEL SLDEQSSSYASSHSDSEDDGVGAEEKWD PARGAVHSTPKGDAVANHVPA 2862  
DSDSDSEL SLDE SSSYASSH+SDSEDDG AE+KW+PA G HSTPK DA+ANHVPA

Sbjct: 2818 PDSDSDSEL SLDEHSSSYASSHTSDSEDDGGEAEDKWNPA GGPAGHSTPKADALANHVPA 2877

Query: 2863 WPDQSLAESDSEDPGKPRKLVETKVSVELHREEQSHRGEYPPDQESGGAAR---LASS 2919  
WPD+SLA SDSE+ +P LKLVETKVSVELHR+ QG+H G+ P D ESG A+ + SS

Sbjct: 2878 WPDES LAGSDSEELDT EPHLKLVETKVSVELHRQAQGNHCGDRPSDPESGVLAKPVAVLSS 2937

Query: 2920 QPPEQRKGILKNKVITYPPPLTLTEQTLKGRLREKLADCEQSPTSSRTSSLGSG----GPD 2975  
QP EQRK GILKNKVITYPPPL EQ LK RLREKLADCEQSPTSSRTSSLGSG D

Sbjct: 2938 QPQEQRKGILKNKVITYPPPLP--EQPLKSRLREKLADCEQSPTSSRTSSLGSGDGVHATD 2995

Query: 2976 CAITVKSPGREPGRDHLNGVAMNVRTGSAQADGSDSEKP 3014  
C IT+K+P REPGR+HLNGVAMNVRTGSAQA+GSDSEKP

Sbjct: 2996 CVITIKTPRREPGRHLNGVAMNVRTGSAQANGSDSEKP 3034



FIG. 6 Continued

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
YVTHSDNFPFGRIPAYODVSHYFTEERENELQLVNNOTCELRLEKEDNHR  
YVTHSDNFPFGRIPAYODVSHYFTEERENELQLVNNOTCELRLEKEDNHR  
YVTHSDNFPFGRIPAYODVSHYFTEERENELQLVNNOTCELRLEKEDNHR

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
PLVSLMLVTEGCHSVTAQVLRVYITTELANCSTVLENNMWTEFLSPLLGHPFSG  
PLEAMMEVSDGCHSVTAQVLRVYITTELANCSTVLENNMWTEFLSPLLGHPFSG  
PLEAMMEVSDGCHSVTAQVLRVYITTELANCSTVLENNMWTEFLSPLLGHPFSG

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
VAAVLATPTDVFPHIGHNTDVGCTLVHVSFALAPRGAGACAAFWFSSEELGECMFC  
VAAVLATPTDVFPHIGHNTDVGCTLVHVSFALAPRGAGACAAFWFSSEELGECMFC  
VAAVLATPTDVFPHIGHNTDVGCTLVHVSFALAPRGAGACAAFWFSSEELGECMFC

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
REAAIAARELLDVLPDENHGRKPEENTHEDSVLRFDSSAPFLANASTLFEPIQVIAE  
REAAIAARELLDVLPDENHGRKPEENTHEDSVLRFDSSAPFLANASTLFEPIQVIAE  
REAAIAARELLDVLPDENHGRKPEENTHEDSVLRFDSSAPFLANASTLFEPIQVIAE

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
LRGCPDPTGDCCTHTELETSNPRNGAAARKEGCVTVVRPRPTDEEDSETEADNR  
LRGCPDPTGDCCTHTELETSNPRNGAAARKEGCVTVVRPRPTDEEDSETEADNR  
LRGCPDPTGDCCTHTELETSNPRNGAAARKEGCVTVVRPRPTDEEDSETEADNR

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
CVPVWGGGTTHAPNGRRQCTAGAGCGRDEVAARSTFPPSFVMEGLRDRPHLT  
CVPVWGGGTTHAPNGRRQCTAGAGCGRDEVAARSTFPPSFVMEGLRDRPHLT  
CVPVWGGGTTHAPNGRRQCTAGAGCGRDEVAARSTFPPSFVMEGLRDRPHLT

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
VLSATVQPSRLFFVHGLMENNHLALEAGVRLTETDESSIVSFTVPHHEDH  
VLSATVQPSRLFFVHGLMENNHLALEAGVRLTETDESSIVSFTVPHHEDH  
VLSATVQPSRLFFVHGLMENNHLALEAGVRLTETDESSIVSFTVPHHEDH

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
QWTHHRRTHHRTDALGGAQOFKEDVAVSVODNVAARFQAEIHHYXAAAIVC  
QWTHHRRTHHRTDALGGAQOFKEDVAVSVODNVAARFQAEIHHYXAAAIVC  
QWTHHRRTHHRTDALGGAQOFKEDVAVSVODNVAARFQAEIHHYXAAAIVC

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
TSKRRLLTGLPGLLOOVNLPENFVSRRDTHHARDLHIGERVLMAAFANAGTTAV  
TSKRRLLTGLPGLLOOVNLPENFVSRRDTHHARDLHIGERVLMAAFANAGTTAV  
TSKRRLLTGLPGLLOOVNLPENFVSRRDTHHARDLHIGERVLMAAFANAGTTAV

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
FQKSHFPAAGPCKNGLSERSWGGGSDFTGFGGSDRLTAAHYHFGNGTSDDFC  
FQKSHFPAAGPCKNGLSERSWGGGSDFTGFGGSDRLTAAHYHFGNGTSDDFC  
FQKSHFPAAGPCKNGLSERSWGGGSDFTGFGGSDRLTAAHYHFGNGTSDDFC

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
NDPWPVYVWYLLSFTNATKTVLQVQLPHVVLCKEDDCLSVTGRASCHAVHDEL  
NDPWPVYVWYLLSFTNATKTVLQVQLPHVVLCKEDDCLSVTGRASCHAVHDEL  
NDPWPVYVWYLLSFTNATKTVLQVQLPHVVLCKEDDCLSVTGRASCHAVHDEL

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
DQMTSEDRWDERRATQEEPGRGHSTFSTSTNTFDTMASSSEGLERKHSHV  
DQMTSEDRWDERRATQEEPGRGHSTFSTSTNTFDTMASSSEGLERKHSHV  
DQMTSEDRWDERRATQEEPGRGHSTFSTSTNTFDTMASSSEGLERKHSHV

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
GPPSSNEEGPQLVCEVGVWTFFFGSSALPPPSSHANNVEFTVINDCAGFPFP  
GPPSSNEEGPQLVCEVGVWTFFFGSSALPPPSSHANNVEFTVINDCAGFPFP  
GPPSSNEEGPQLVCEVGVWTFFFGSSALPPPSSHANNVEFTVINDCAGFPFP

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
HANXELWQVSTWVPHVPGVYSILLNPNQONSRHLQGFHGVTEKSYDEE  
HANXELWQVSTWVPHVPGVYSILLNPNQONSRHLQGFHGVTEKSYDEE  
HANXELWQVSTWVPHVPGVYSILLNPNQONSRHLQGFHGVTEKSYDEE

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
HCHRMQQQPPGWSSTISGNDHCEGFPNNKSSGCHKFFHTRPSSEGLCP  
HCHRMQQQPPGWSSTISGNDHCEGFPNNKSSGCHKFFHTRPSSEGLCP  
HCHRMQQQPPGWSSTISGNDHCEGFPNNKSSGCHKFFHTRPSSEGLCP

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
DCHVTERSTAPHSDGPPPHAGPPOCHSSTSPFAEYASGRVVDONPPSLRSN  
DCHVTERSTAPHSDGPPPHAGPPOCHSSTSPFAEYASGRVVDONPPSLRSN  
DCHVTERSTAPHSDGPPPHAGPPOCHSSTSPFAEYASGRVVDONPPSLRSN

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
WWPOTKFOVLAIVCPKFAELRGTGAVRLDESHWLEDFHCTPARELSLLEG  
WWPOTKFOVLAIVCPKFAELRGTGAVRLDESHWLEDFHCTPARELSLLEG  
WWPOTKFOVLAIVCPKFAELRGTGAVRLDESHWLEDFHCTPARELSLLEG

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
ELKALITVEKQKQREVEYTCQDHYFSQVHVYARLAYEAFESHNNGTAT  
ELKALITVEKQKQREVEYTCQDHYFSQVHVYARLAYEAFESHNNGTAT  
ELKALITVEKQKQREVEYTCQDHYFSQVHVYARLAYEAFESHNNGTAT

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
QGRHNNELWALALAPSTGDLWAAGGRAPHSFGSAGLHLEEAATMARHMDLT  
QGRHNNELWALALAPSTGDLWAAGGRAPHSFGSAGLHLEEAATMARHMDLT  
QGRHNNELWALALAPSTGDLWAAGGRAPHSFGSAGLHLEEAATMARHMDLT

Rat\_MEGF2  
Assembled\_CDS  
Mouse\_Celr  
YLVNFGVTPHLLSRRMSQPSSESQAHHYPRYHNSIFCQQA- AWDPTHVLL...S  
YLVNFGVTPHLLSRRMSQPSSESQAHHYPRYHNSIFCQQA- AWDPTHVLL...S  
YLVNFGVTPHLLSRRMSQPSSESQAHHYPRYHNSIFCQQA- AWDPTHVLL...S

*(The following are the names of the persons who have been elected to the various offices of the Association, as reported by the Secretary.)*

[illegible]

FIG. 7

ATGGAGTTTGTGCGGGCGCTGTGGCTGGGCCTGGCGCTGGCGCTGGGGCCGGGGTCCGCGGGGGGC  
 CACCCTCAGCCGTGCGGGCTCCTGGCGCGCCTCGGGGGCTCCGTGCGCCTGGGCGCCCTCCTGCCCC  
 GCGCGCCTCTCGCCCGCGCCCGCGCCCGCGCCCTGGCCCGGGCCGCCCTGGCGCGCGGCTGCC  
 GCACAACCTGAGCTTGGAGCTGGTGGTGGCGCGCCCCCGCCCGCGACCCCGCCTCGCTGACCCGC  
 GGCTGTGCCAGGCGCTGGTGCCTCCGGGGCGTGGCGGCCCTGCTCGCCTTTCCCGAGGCTCGGCCCG  
 AGCTGCTGCAGCTGCACTTCTGGCGGGCGGCCACCGAGACCCCCGTGCTCAGCCTGCTGCGGCGGG  
 AGGCGCGCGCGCCCTCGAGCCCCGAACCCATTCCACCTGCAGCTGCACTGGGCCAGCCCCCTGG  
 AGACGCTGCTGGATGTGCTGGTGGCGGTGCTGCAGGCGCACGCCTGGGAAGACGTCGGCCTGGCCC  
 TGTGCCGCACTCAGGACCCCGCGGGCCTGGTGGCCCTCTGGACAAGCCGGGCTGGCCGGCCCCCAC  
 AGCTGGTCTTGACCTAAGCCGGCGGGACACGGGAGATGCAGGACTGCGGGCACGCCTGGCCCCGA  
 TGGCGGGCCAGTGGGGGGTGAAGCACCGGTACCCGCGGGCGTCTCCTCGGCTGTGACATCGCCC  
 GTGCCCCGTGGGTGCTGGAGGCCGTACCTCCCGGCCCCCACTGGCTGTTGGGGACACCACTGCCGCC  
 CAAGGCCCTGCCACCGCGGGGCTGCCACAGGGCTGCTGGCGCTGGGCGAGGTGGCACGACCCCC  
 GCTGGAGGCCGCCATCCATGACATTGTGCAACTGGTGGCCCGGGCGCTGGGCACTGCGGCCAGGT  
 GCAGCCGAAGCGAGCCCTCCTCCCCGCCCCGGTCAACTGCGGGGACCTGCAGCCGGCGGGGCCCGA  
 GTCCCCGGGGCGCTTCTTGGCACGGTTCCTGGCCAACACGTCTTCCAGGGCCGCAACGGGCCCGGTG  
 TGGGTGACAGGCAGCTCCCCAGACGAAGACGGGCAGTGCCAGCGGGGAGCTGTGCCTGGACCCT  
 GGCACCAACGACTCGGCCACCCCTGGACGCACTGTTCCGCCGCGCTGGCCAACGGCTCAGCGCCCCGT  
 GCCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCC  
 TTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACC  
 GGCCTGGTGGGGACCTGCTGGCCGGCCGGGGCCACATGGCGGTACCCAGCTTCAGTATCAACTCC  
 GCCCCGTACAGGTGGTGGACTTCACCAAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGGG  
 CACGGGACACGGCCCTCACCATCGGTGCCTTTATGTGGCCCTGCACTGGTCCACGTGGCTGGGCGT  
 CTTTGGCGCCCTGCACCTCACCGCGCTCTTCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCCTC  
 ACGCCACGTGGCCGCAACCGCACACCGCTCTTCTCTACTCTCAGCCCTCAACCTGTGCTACGCCA  
 TCCTCTTCAGACGCAACCGTGTCCAGCAAGACGCCAAGTGCCCCACGGGCCCGCTGCTCATGAACCT  
 CTGGGCCATCTTCTGCTGCTGGTGTCTTCCAGCTACACGGCCAACCTGGCTGCCGTATGGTCCGG  
 GACAAGACCTTCGAGGAGCTGTGGGGATCCACGACCCCCAAGGGCTTCCGCTTCGGCACCGTGTGG  
 GAGAGCAGCGCCGAGGCGTACATCAAGAAGAGCTTCCCCGACATGCACGCACACATGCGGCGCCAC  
 AGCGCGCCACCAACGCCCCGCGGCGTCCCATGCTCACGAGCGACCCCCCAAGCTCAACGCCCTTC  
 ATCATGGACAAGTCGCTCCTGGACTACGAGGTCTCCATCGACGCCGACTGCAAACCTGCTGACCGTGG  
 GAAAGCCCTTCGCCATTGAGGGCTATGGGATCGGACTGCCCCAGAACTCGCCGCTCACCTOCAACCT  
 GTCCGAGTTCATCAGCCGCTACAAGTCTTCCGGCTTCATCGACCTGCTCCACGACAAGTGGTACAAG  
 ATGGTGCCTTGCGGCAAGCGGGTCTTGGCGTTACAGAGACCCTGCAGATGAGCATCTACCACTTCG  
 CGGGCCTCTTCGTGTTGCTGTGCCTGGGCCTGGGCAGCGCTCTGCTCAGCTCGCTGGGGGAGCACGC  
 CTTCTTCCGCTGGCGCTGCCGCGCATCCGCAAGGGGAGCAGGCTGCAGTACTGGCTGCACACCAGC  
 CAGAAAATCCACCGCGCCCTCAACACGGAGCCACAGAGGGGTGGAAGGAGGAGACGGCAGAGGC  
 GGAGCCCAGCGGCCCGGAGGTGGAGCAGCAGCAGCAGCAGGACCAGCCAACGGCTCCGGAGG  
 GCTGGAAACGGGCGCGCCGGGCGGTGGACAAGGAGCGCCGCGTGGCGCTTCTGCTGGAGCCCCCG  
 TGGTTGTGGACCCGAAGCGGACCGGAGGCGGAGGCTGCGCCGCGAGAGGGCCCCCTGCTGGCTGT  
 GCTCCTACGGCCGCCCGCCCGCCGCAAGGCCACGGGGGCCCCCCAGCCCGGGGAGCTGCAGGAGC  
 TGGAGCGCCGCATCGAAGTCGCGCGTGAGCGGCTCCGCCAGGCCCTGGTGGCGCGCGGCCAGCTCC  
 TGGCACAGCTCGGGGACAGCGCACGTACCGGCCCTCGGCGCTTGCTTCAGGCCAGAGCGGCCCCCCG  
 CGGAGGCCCCACCACTCTGGCCGACCGGGGAGCCAGGAATGA

FIG. 8

MEFVRALWLGLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARAALAPRLPH  
NLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVLSSLRREARAP  
LGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTLQDPGGLVALWTSRAGRPPQLVLDLS  
RRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTFLPPKALFTAGLP  
PGLLALGEVARPPLEAAIHDIQVLVARALGSAAQVQPKRALLPAPVNCGLQAGPESPGRFLARFLANT  
SFQGRTPGVWVTGSSPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER  
LAEDTPDFELYLVDGDKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTSPFFSTSLGI  
MVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFTVYEWRSPLYGLTPRGRNRSTVFSYSSALNLC  
YAILFRRTVSSKTPKCPTGRLLMNLWAFCLLVLSYTANLAAMVGDKITFEELSGIHDPKGFRFGTVWE  
SSAEAYIKKSFPDMHAHMRRHSAPTTPRGVAMLTSDPPKLNAFIMDKSLDYEVSIDADCKLLTVGKPF  
AIEGYGIGLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKRVPFAVTETLQMSIYHFAGLFVLLC  
LGLGSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRAFNTEPPEGSKEETAEEAPSGPEVEQQQQ  
QQDQPTAPEGWKRARRAVDKERRVRFLLEPAVVVAPEADAEAEAAPREGPVWLCSYGRPPAARPTGAP  
QPGELQELERRIEVARERLRQALVRRGQLLAQLGDSARHRPRRLQARAAPAEAPPHSGRPGSQE

FIG. 9

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(5) = 0.0

Identities = 928/1076 (86%), Positives = 928/1076 (86%), Strand = Plus / Plus

Query: 788 CACTGCCGCCCAAGGCCCTGCCACCGCGGGCTGCCACCAGGGCTGCTGGCGCTGGGCG 847  
C CTGCC CC A G CCTG CCA C CG CT CCA GC C GGC C G G G  
Sbjct: 22736 CCCTGCC-CCTAGGTTCCTGGCCAACACGTC-CTTCCAGGGCCGCA-CGGGCCCCGTGTG 22792

Query: 848 AGGTGGCAGC-ACCCCCGCTGG-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGG 901  
GGTG CA G A C CC C GG A C G C C C C T A TGTG A C T G  
Sbjct: 22793 -GGTGACAGGCAGCTCC-CAGGTACACATGTCTCGGCACTTTAAGGTGTGGAGCCT-TCG 22849

Query: 902 CCGGGGCGCT-GGGCAGTGCGGGCCAGGTGCAGCCGAAGCGAGCCCTCCTCCCCGCCCCG 960  
CC GG C C GGG G C G CC GG CA C G G AGC C C GCC G  
Sbjct: 22850 CCGGGACCCACGGGGCGCCCCGGCCTGGGCCA-CGGTGGGCAGCTGGCGGGACGGCCA-G 22907

Query: 961 GTCAACTGCGGGGACCTGCAGCCGGCCGGGCCCCGAGTCCCCGGGGCG-CTTCTTGGCAGC 1019  
T ACT GG ACC G AG G C GC CG G CCCCC C C TG C G  
Sbjct: 22908 CTGGACTT--GGAACCGGGAGGTGCCTCTGCAGC-GCCCCCGCCCCACAGGGTGGCCAG 22964

Query: 1020 GTTCCTGGCC-AA-CA-CGTCTTCCAGGGCCCGCACGGGC-CCCCTGTGGGTGACAGGCA 1075  
GT CTGGCC AA C CGT T A GC G G C CCC T TG GT G C  
Sbjct: 22965 GT--CTGGCCCAAGCTGCGTG-TGTAACGCTGTTGGAACACCCATTTGTGTTT--GCCC 23019

Query: 1076 GCTCCCCAGACGAAGACGGGCAGTGCCACGCGGGGAGCTGTGCCTGGACCCCTGGCACCA 1135  
G CCAGACGAAGACGGGCAGTGCCACGCGGGGAGCTGTGCCTGGACCCCTGGCACCA  
Sbjct: 23020 GTGATCCAGACGAAGACGGGCAGTGCCACGCGGGGAGCTGTGCCTGGACCCCTGGCACCA 23079

Query: 1136 ACGACTCGGCCACCCCTGGACGCACTGTTTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG 1195  
ACGACTCGGCCACCCCTGGACGCACTGTTTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG  
Sbjct: 23080 ACGACTCGGCCACCCCTGGACGCACTGTTTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG 23139

Query: 1196 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 1255  
CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA  
Sbjct: 23140 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 23199

Query: 1256 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 1315  
CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG  
Sbjct: 23200 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 23259

Query: 1316 GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA 1375  
GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA  
Sbjct: 23260 GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCA 23319

Query: 1376 GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA 1435  
GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA  
Sbjct: 23320 GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCA 23379

Query: 1436 CCAGCCTGGGCATCATGGTGCGGGACGGGACACGGCCTCACCATCGGTGCCTTTATGT 1495  
CCAGCCTGGGCATCATGGTGCGGGACGGGACACGGCCTCACCATCGGTGCCTTTATGT  
Sbjct: 23380 CCAGCCTGGGCATCATGGTGCGGGACGGGACACGGCCTCACCATCGGTGCCTTTATGT 23439

Query: 1496 GGCCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCAGCGCTCT 1555  
GGCCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCAGCGCTCT

# FIG. 9 Continued

Sbjct: 23440 GGCCCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTACCGCGCTCT 23499

Query: 1556 TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 1615  
TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA

Sbjct: 23500 TCCTCACCGTGTACGAGTGGCGTAGCCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCA 23559

Query: 1616 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 1675  
GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA

Sbjct: 23560 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 23619

Query: 1676 CCGTGTCAGCAAGACGCCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA 1735  
CCGTGTCAGCAAGACGCCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA

Sbjct: 23620 CCGTGTCAGCAAGACGCCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA 23679

Query: 1736 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTCATGGTCGGGG 1795  
TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTCATGGTCGGGG

Sbjct: 23680 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTCATGGTCGGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTGCGGGGATCCACGACCCCAAGGGCTTCCGCTTCGGCACCG 1855  
ACAAGACCTTCGAGGAGCTGTGCGGGGATCCACGACCCCAAGG C GC TCGG

Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTGCGGGGATCCACGACCCCAAGGTGGGCGGCCTCGGGGGGC 23799

Query: 1856 TGTGGGAG 1863  
TG GGG G

Sbjct: 23800 TGCGGGTG 23807



FIG. 10

Score = 2426 (854.0 bits), Expect = 0.0, Sum P(2) = 0.0  
Identities = 463/474 (97%), Positives = 464/474 (97%), Frame = +1

Query: 1063 WVTGSSPDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 1242  
+V PDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER  
Sbjct: 427 FVFARDPDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 486

Query: 1243 LAEDTPDFELYLVDGDKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422  
LAEDTPDFELYLVDGDKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS  
Sbjct: 487 LAEDTPDFELYLVDGDKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query: 1423 PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVEYWRSPYGLTPR 1602  
PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVEYWRSPYGLTPR  
Sbjct: 547 PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVEYWRSPYGLTPR 606

Query: 1603 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAIIFCLLVLSSTANLAA 1782  
GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAIIFCLLVLSSTANLAA  
Sbjct: 607 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAIIFCLLVLSSTANLAA 666

Query: 1783 VMVGDKTFEELSGIHDPK-----GFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP 1944  
VMVGDKTFEELSGIHDPK GFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP  
Sbjct: 667 VMVGDKTFEELSGIHDPKLHHPAQGFRFGTVWESSAEAYIKKSFPDMHAMRRHSAPTTP 726

Query: 1945 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN 2124  
RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN  
Sbjct: 727 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN 786

Query: 2125 LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRFAVTETLQMSIYHFAGLFVLLCLGLGSAL 2304  
LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRFAVTETLQMSIYHFAGLFVLLCLGLGSAL  
Sbjct: 787 LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRFAVTETLQMSIYHFAGLFVLLCLGLGSAL 846

Query: 2305 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 2466  
LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP  
Sbjct: 847 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 900

FIG. 11

Gltamate\_Receptor\_RAT\_AAD4165 MRRSLWVLLSRCLLLPFPCCALVLAGVPSSSSHPPQPCQLKCHAVRCAHLPQWTT  
Gltamate\_Receptor\_Human\_06039 MEFVRALWLG--LALALGP-----GS--AGGHPQPCCVLARLGGSVRLGALLPR--  
21659259\_EXT MEFVRALWLG--LALALGP-----GS--AGGHPQPCCVLARLGGSVRLGALLPR--

Gltamate\_Receptor\_RAT\_AAD4165 APRAASRAQEGGRRAAQEDDPESGTWRPPAPSSQGARWLGSAIHGPGPPGSRKLGEAGAGAE  
Gltamate\_Receptor\_Human\_06039 APLARARA---RAALAR---AALAPR---  
21659259\_EXT APLARARA---RAALAR---AALAPR---

Gltamate\_Receptor\_RAT\_AAD4165 TLWPRDALLFAVENLNRVEGLLPYNLSLEVMIAEAGLGDLPLMPFSSPSSPWSSDFEF  
Gltamate\_Receptor\_Human\_06039 -----LPHNLSLELVVAAPP-----ARDPASL  
21659259\_EXT -----LPHNLSLELVVAAPP-----ARDPASL

Gltamate\_Receptor\_RAT\_AAD4165 LQSCHTAVVGVSAALLAFPOSQGEELDLSSSVLHIVLSREFF--PRESQNLHL  
Gltamate\_Receptor\_Human\_06039 TRGLCQALVPPGVAAALLAFPEARPELLQLHFLAAATETPVL SLLREEARAPLGAPNPFHL  
21659259\_EXT TRGLCQALVPPGVAAALLAFPEARPELLQLHFLAAATETPVL SLLREEARAPLGAPNPFHL

Gltamate\_Receptor\_RAT\_AAD4165 QLSLENSLSADADWTVSLLTMNNYNFSLLLCQEDWNI TDFLLTENNNSKFHLESVIN  
Gltamate\_Receptor\_Human\_06039 QLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGI VALWTSRAG--RPPQLVLDLS  
21659259\_EXT QLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGI VALWTSRAG--RPPQLVLDLS

Gltamate\_Receptor\_RAT\_AAD4165 ANLSTIKDLSFLQVQMDNR--NSTPTMFFGCDSDSIRQFEMSTQFGSPPELHWL  
Gltamate\_Receptor\_Human\_06039 RRD TGDAGLRLAPMAAPVGG EAPVPAAVLLGCDIARARRVLEA-----PPGPHWLL  
21659259\_EXT RRD TGDAGLRLAPMAAPVGG EAPVPAAVLLGCDIARARRVLEA-----VPPGPHWLL

Gltamate\_Receptor\_RAT\_AAD4165 GDSQNV EELRTGLPLGLAHKTIQSVFYYQDAELVARAVATMQLALIPST  
Gltamate\_Receptor\_Human\_06039 GTPLPPKALPTAGLPGLLALGEVARPPLEAAIHDIVQLVARALGSAAQVQPKRALLPAP  
21659259\_EXT GTPLPPKALPTAGLPGLLALGEVARPPLEAAIHDIVQLVARALGSAAQVQPKRALLPAP

Gltamate\_Receptor\_RAT\_AAD4165 VNCMDKKTINLSQQLSRFLANTFRGLGSGKVKGSNLSSENFFVNLQHDPMK  
Gltamate\_Receptor\_Human\_06039 VNCGLDLPAGFESPGRFLARFLANTSFQGRTPGVVVTGSSQHMSRHEKWSLRDRRKA  
21659259\_EXT VNCGLDLPAGFESPGRFLARFLANTSFQGRTPGVVVTGSSQHMSRHEKWSLRDRRKA

Gltamate\_Receptor\_RAT\_AAD4165 PMWTRGSGWQGRIVVSGIWP EQAQKHKTHFQHPNKLHVRVTL EHPFVETREVD  
Gltamate\_Receptor\_Human\_06039 PAWATGSGWRDQGDPE--GASARPPPPQGAQVWP KLRVTL EHPFVETREVD  
21659259\_EXT PAWATGSGWRDQGDPE--GASARPPPPQGAQVWP KLRVTL EHPFVETREVD

Gltamate\_Receptor\_RAT\_AAD4165 LCPAGQLCLDPMTNDS SMLDR LFS SLHSSNDVPIKFKECCYGYCIDLLEQLAEDMNFDF  
Gltamate\_Receptor\_Human\_06039 QCPAGQLCLDPGTNDS SATLDALFAALANG--SAPRALRECCYGYCIDLLERLAEDTPDF  
21659259\_EXT QCPAGQLCLDPGTNDS SATLDALFAALANG--SAPRALRECCYGYCIDLLERLAEDTPDF

Gltamate\_Receptor\_RAT\_AAD4165 DLYVGDGKYGAWRNGHWTGLVGDLLSTIANMAVT SFSINARSQVDFTSPPFFSTSLGI  
Gltamate\_Receptor\_Human\_06039 ELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVT SFSINARSQVDFTSPPFFSTSLGI  
21659259\_EXT ELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVT SFSINARSQVDFTSPPFFSTSLGI

Gltamate\_Receptor\_RAT\_AAD4165 EVRTIDTAAPIGAFMWPLHWSWLVGLFVALHHTAFELTVEWESPGCTPGRNRNKVFS  
Gltamate\_Receptor\_Human\_06039 MVRARDTASPIGAFMWPLHWS TWLGVFAALHLTALFLTVYEWRSYGLTPEGRNRSTVFS  
21659259\_EXT MVRARDTASPIGAFMWPLHWS TWLGVFAALHLTALFLTVYEWRSYGLTPEGRNRSTVFS

Gltamate\_Receptor\_RAT\_AAD4165 YSSALNLCYAILFGRTAAIKPPECWTGFLMLNLWAI FCLLCLSYTANLAAMVGDKTFE  
Gltamate\_Receptor\_Human\_06039 YSSALNLCYAILFRRTVSSKTPKCPTGRLLMLNLWAI FCLLVLSY TANLAAMVGDKTFE  
21659259\_EXT YSSALNLCYAILFRRTVSSKTPKCPTGRLLMLNLWAI FCLLVLSY TANLAAMVGDKTFE

Gltamate\_Receptor\_RAT\_AAD4165 ELSGIHD PKLHHPSSQGRFGTVRES SAEYIKESFPDMHMHMRHSAPTTPRGVAMLTSD  
Gltamate\_Receptor\_Human\_06039 ELSGIHD PKLHHPAGGFRFGTVWESSAEAYIKESFPDMHMHMRHSAPTTPRGVAMLTSD  
21659259\_EXT ELSGIHD PK-----GFRFGTVWESSAEAYIKESFPDMHMHMRHSAPTTPRGVAMLTSD

Gltamate\_Receptor\_RAT\_AAD4165 PEKLD AFIMDHALLDYEVSIDADCKLLTVGKPPFAIEGYGIGLPNSPLTSHSELISQK  
Gltamate\_Receptor\_Human\_06039 PPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPFAIEGYGIGLPQNSPLTSHSELISRYK  
21659259\_EXT PPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPFAIEGYGIGLPQNSPLTSHSELISRYK

Gltamate\_Receptor\_RAT\_AAD4165 SHGFMDLHDKWYVVPCKGRSFAVTETLQMGIKHFSGLFVLLCGLSGLGEHIV  
Gltamate\_Receptor\_Human\_06039 SSGFIDLHDKWYVMPCKGRVFAVTETLQMSIYHFAGLFVLLCGLGSAISSLGEHAF  
21659259\_EXT SSGFIDLHDKWYVMPCKGRVFAVTETLQMSIYHFAGLFVLLCGLGSAISSLGEHAF

Gltamate\_Receptor\_RAT\_AAD4165 HRLLLPRIKNSQLQVWLHTSQFHRALNTSFVEEKQPSEKTKRVERRWRWICKTEGD  
Gltamate\_Receptor\_Human\_06039 FRLALPRIREGSRLQVWLHTSQKIHRALNTEPPEGSS--KEETAEAEP-----GP--  
21659259\_EXT FRLALPRIREGSRLQVWLHTSQKIHRALNTEPPEGSS--KEETAEAEP-----GP--

Gltamate\_Receptor\_RAT\_AAD4165 SEISLFPSSNLGPQQLMVNTSNLSHNDNQRYIFND EEQNQLGTQAHQD IPLQRREL  
Gltamate\_Receptor\_Human\_06039 -EEEQQQQQQDQPTAPEGWKRARRAVKEERVRFLLEPQVVVAPEADAEAEAA--REG  
21659259\_EXT -EEEQQQQQQDQPTAPEGWKRARRAVKEERVRFLLEPQVVVAPEADAEAEAA--REG

Gltamate\_Receptor\_RAT\_AAD4165 PASLTNENRADS LNVTRSSVIQELS ELEKQIQWIRQELQLASR--TELEEQKINETCE  
Gltamate\_Receptor\_Human\_06039 PVWLCSYGRPPAARP TGAPQPGELQELERRTEARERERQATVRGQLLAQLGDAAHRP  
21659259\_EXT PVWLCSYGRPPAARP TGAPQPGELQELERRTEARERERQATVRGQLLAQLGDAAHRP

Gltamate\_Receptor\_RAT\_AAD4165 S-----  
Gltamate\_Receptor\_Human\_06039 -----  
21659259\_EXT RRL LQARAAPAEAPPHSGRPGSQE

FIG. 12

ATGGAGTTTGTGCGGGCGCTGTGGCTGGGCTGGCGCTGGCGCTGGGGCCGGGGTCCGCGGGGGG  
CACCTCAGCCGTGCGGCGTCTGGCGCGCTCGGGGGCTCCGTGCGCCTGGGCGCCCTCCTGCCCC  
GCGCGCCTCTCGCCCGCGCCCGCGCCCGCCCTGGCCCGGGCCGCGCTGGCGCCGCGGCTGCC  
GCACAACCTGAGCTTGGAGCTGGTGGTGGCGCGCCCCCGCCGCGACCCCGCCTCGCTGACCCGC  
GGCCTGTGCCAGGCGCTGGTGCCTCCGGGCGTGGCGGCCCTGCTCGCCTTTCCCGAGGCTCGGCCCG  
AGCTGCTGCAGCTGCACCTTCTGGCGGCGGCCACCGAGACCCCGTGTCTCAGCCTGCTGCGGCGGG  
AGGCGCGCGCGCCCTCGGAGCCCGAACCATTCCACCTGCAGCTGCACTGGGCCAGCCCCCTGG  
AGACGCTGCTGGATGTGCTGGTGGCGGTGCTGCAGGCGCACGCTGGGAAGACGTGGGCTGGCCC  
TGTGCCCACTCAGGACCCCGCGGCCCTGGTGGCCCTCTGGACAAGCCGGGCTGGCCGGCCCCAC  
AGCTGGTCTGGACCTAAGCCGGCGGGACACGGGAGATGCAGGACTGCGGGCACGCTGGCCCCGA  
TGGCGGCGCCAGTGGGGGGTGAAGCACCGGTACCCGCGGCGGTCTCTCGGCTGTGACATCGCCC  
GTGCCCGTGGGTGCTGGAGGCCGTACCTCCCGGCCCACTGGCTGTTGGGGACACCACTGCCGCC  
CAAGGCCCTGCCACCCGCGGGGCTGCCACAGGGCTGCTGGCGCTGGGCGAGGTGGCACGACCCCG  
GCTGGAGGCCCGCATCCATGACATTGTGCAACTGGTGGCCCGGGCGCTGGGCAGTGCGGCCAGGT  
GCAGCCGAAGCGAGCCCTCTCCCGGCCCGGTCAACTGCGGGGACCTGCAGCCGGCCGGGCCCCGA  
GTCCCCGGGGCGCTTCTTGGCACGGTTCCTGGCCAACAGTCTTCCAGGGCCGACCGGGCCCCGTG  
TGGGTGACAGGCACTCCCAAGACGAAGACGGGCACTGCCAGCGGGGCACTGTGCTTGGACCTT  
GGACCAACGACTCGGCCACCTGGACGCACTGTTCCGCGCGTGGCCAACGGGCTCAGCGCCCCGT  
GCCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCC  
TTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACCGCCGCTGGACC  
GGCCTGGTGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTCAACAGCTTCAGTATCAACTCC  
GCCCCGTCAAGGTGGTGGACTTCACAGCCCCCTTCTTCTCCACAGCCTGGGCATCATGGTGGGG  
CACGGGACACGGCCTCACCATCGGTGCCTTTATGTGGCCCCCTGCACTGGTCCACGTGGCTGGGCGT  
CTTTGCGGCCCTGCACCTCACCGCGCTCTTCTCACCGTGTACGAGTGGCCTAGCCCCCTACGGCCTC  
ACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCTACTCCTCAGCCCTCAACCTGTGCTACGCCA  
TCCTCTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGGCCACCGGGCCGCTGCTCATGAACCT  
CTGGGCCATCTTCTGCTGTGGTGTGTCCAGCTACACGGCCAACCTGGCTGCCGTGCTGGTGGG  
GACAAGACCTTCGAGGAGCTGTGGGGATCCAAGACCCCAAGCTGCACACCCGGGCGCAGGGCTT  
CCGCTTCGGCACCGTGTGGGAGAGCAGCGCCGAGGCGTACATCAAGAAGAGCTTCCCCGACATGCA  
CGCACACATGCGGCGCCACAGCGCGCCACACGCCCCGCGGCGTCCGCTGCTCAGAGCGACCC  
CCCCAAGCTCAACGCCCTTCATCATGGACAAGTGGCTCTGGACTACGAGGTCTCCATCGACGCCGAC  
TGAAACTGCTGACCGTGGGAAAGCCCTTCGCCATTGAGGGCTATGGGATCGGACTGCCCCAGAAC  
TCGCCGCTCACCTCCAACCTGTCCGAGTTCATCAGCCGCTACAAGTCTCCGGCTTCATCGACCTGT  
CCACGACAAGTGGTACAAGATGGTGCCTTGGCGCAAGCGGGTCTTTGCGGTTACAGAGACCTGCA  
GATGAGCATCTACCACTTCGCGGGCCTCTTCGTGTTGCTGTGCCTGGGCCCTGGGCAAGCTGTGCTC  
AGCTCGCTGGGCGAGCACGCTTCTTCCGCTGGCGCTGCCGCGCATCCGCAAGGGGAGCAGGCTG  
CAGTACTGGCTGCACACCAAGCCAGAAAATCCACCGCGCCCTCAACACGGAGCCACAGAGGGGTG  
AAGGAGGAGACGGCAGAGGCGGAGCCAGCGGCCCGAGGTGGAGCAGCAGCAGCAGCAGCAGG  
ACCAGCCAACGGCTCCGGAGGGCTGGAAACGGGCGCGCCGGGCGGTGGACAAGGAGCGCGCGTG  
CGCTTCTGCTGGAGCCCCCGCTGGTGTGGCAACCGAAGCGGACCGCGGAGGCGGAGGCTGCGCCG  
CGAGAGGGCCCCGTCTGGCTGTGCTCTACGGCCCGCCCGCCGCGCAAGGCCACGGGGGGCCCC  
CAGCCCCGGGAGCTGCAGGAGCTGGAGCGCCGATCGAAGTCCGCGGTGAGCGGCTCCGCCAGGCC  
CTGGTGGCGCGCGGCCAGCTCTGGCACAGCTCGGGGACAGCGCACGTACCGGCCCTCGGCGCTTG  
CTTCAGGCCAGAGCGGCCCCCGCGGAGGCCCCACCACTCTGGCCGACCGGGGAGCCAGGAATGA

FIG. 14

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(3) = 0.0  
Identities = 948/1107 (85%), Positives = 948/1107 (85%), Strand = Plus / Plus

Query: 788 CACTGCCGCCCAAGGCCCTGCCACCGGGGCTGCCACCAGGGCTGCTGGCGCTGGGCG 847  
C CTGCC CC A G CCTG CCA C CG CT CCA GC C GGC C G G G  
Sbjct: 22736 CCCTGCC-CCTAGGTTCTTGGCCAACACGTC-CTTCCAGGGCCGCA-CGGGCCCCGTGTG 22792

Query: 848 AGGTGGCAG-ACCCCCGCTGG-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGG 901  
GGTG CA G A C CC C GG A C G C C C C T A TGTG A C T G  
Sbjct: 22793 -GGTGACAGGCAGCTCC-CAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCT-TCG 22849

Query: 902 CCGGGGCGCT-GGGCAGTGCGGCCAGGTGCAGCCGAAGCGAGCCCTCCTCCCCGCCCCG 960  
CC GG C C GGG G C G CC GG CA C G G AGC C C GCC G  
Sbjct: 22850 CCGGGACCCACGGGGCGCCCCGGCCTGGGCCA-CGGTGGGCAGCTGGCGGGACGGCCA-G 22907

Query: 961 GTCAACTGCGGGGACCTGCAGCCGGCCGGGCCCGAGTCCCCGGGGCG-CTTCTTGGCAG 1019  
T ACT GG ACC G AG G C GC CG G CCCCC C C TG C G  
Sbjct: 22908 CTGGACTT--GGAACCGGGAGGTCCCTCTGCACG-GCCCCCGCCCCACAGGGTGCCCG 22964

Query: 1020 GTTCCTGGCC-AA-CA-CGTCCTTCCAGGGCCGCAAGGGC-CCCCTGTGGGTGACAGGCA 1075  
GT CTGGCC AA C CGT T A GC G G C CCC T TG GT G C  
Sbjct: 22965 GT--CTGGCCCAAGCTGCGTG-TGGTAACGCTGTTGGAACACCCATTGTGTTT--GCCC 23019

Query: 1076 GCTCCCCAGACGAAGACGGGCAGTGGCCAGCGGGGACCTGTGCCTGCACCCCTGGCACCA 1135  
G CCAGACGAAGACGGGCAGTGGCCAGCGGGGACCTGTGCCTGCACCCCTGGCACCA  
Sbjct: 23020 GTGATCCAGACGAAGACGGGCAGTGGCCAGCGGGGACCTGTGCCTGCACCCCTGGCACCA 23079

Query: 1136 ACGACTCGGCCACCCTGGACGCACGTGTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG 1195  
ACGACTCGGCCACCCTGGACGCACGTGTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG  
Sbjct: 23080 ACGACTCGGCCACCCTGGACGCACGTGTCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTG 23139

FIG. 14 Continued

Query: 1196 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 1255  
 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA  
 Sbjct: 23140 CCCTGCGCAAGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 23199

Query: 1256 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGGACG 1315  
 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGGACG  
 Sbjct: 23200 CGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGGACG 23259

Query: 1316 GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCCCACATGGCGGTCACCA 1375  
 GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCCCACATGGCGGTCACCA  
 Sbjct: 23260 GCCGCTGGACCGGCCCTGGTCGGGGACCTGCTGGCCGGCCGGGCCCCACATGGCGGTCACCA 23319

Query: 1376 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA 1435  
 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA  
 Sbjct: 23320 GCTTCAGTATCAACTCCGCCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTTCTCCA 23379

Query: 1436 CCAGCCTGGGCATCATGGTGCGGGGACGGGACACGGCCTCACCCTATCGGTGCCTTTATGT 1495  
 CCAGCCTGGGCATCATGGTGCGGGGACGGGACACGGCCTCACCCTATCGGTGCCTTTATGT  
 Sbjct: 23380 CCAGCCTGGGCATCATGGTGCGGGGACGGGACACGGCCTCACCCTATCGGTGCCTTTATGT 23439

Query: 1496 GGCCCCCTGCACCTGGTCCACGTGGCTGGGCGTCTTTGCGGGCCCTGCACCTCACC GCGCTCT 1555  
 GGCCCCCTGCACCTGGTCCACGTGGCTGGGCGTCTTTGCGGGCCCTGCACCTCACC GCGCTCT  
 Sbjct: 23440 GGCCCCCTGCACCTGGTCCACGTGGCTGGGCGTCTTTGCGGGCCCTGCACCTCACC GCGCTCT 23499

Query: 1556 TCCTCACCCTGTACGAGTGGCGTAGCCCCCTACGGCCTCAGGCCACGTGGCCGCAACCGCA 1615  
 TCCTCACCCTGTACGAGTGGCGTAGCCCCCTACGGCCTCAGGCCACGTGGCCGCAACCGCA  
 Sbjct: 23500 TCCTCACCCTGTACGAGTGGCGTAGCCCCCTACGGCCTCAGGCCACGTGGCCGCAACCGCA 23559

Query: 1616 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 1675  
 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA  
 Sbjct: 23560 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGACGCA 23619

Query: 1676 CCGTGTCAGCAAGACGCCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA 1735  
 CCGTGTCAGCAAGACGCCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA  
 Sbjct: 23620 CCGTGTCAGCAAGACGCCCCAAGTGCCCCACGGGCCGCTGCTCATGAACCTCTGGGCCA 23679

Query: 1736 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTCATGGTCGGGG 1795  
 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTCATGGTCGGGG  
 Sbjct: 23680 TCTTCTGCCTGCTGGTGCTGTCCAGCTACACGGCCAACCTGGCTGCCGTCATGGTCGGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCCAAGCTGCACCACC-CGGCGCAG 1854  
 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCCAAG TG C CC CGG G G  
 Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCCAAGGTGGGCGGCCTCGG-G--G 23796

Query: 1855 GGCTTCCGCTTCGGCACCGTGTGGGAGAGCAGCG-CCGAGG 1894  
 GGCT C G T GGC G G GGG AGC G G CC GG  
 Sbjct: 23797 GGCTGCGGGT--GGCCTTGGG-GGGCTAGCGGTGGCCCCGG 23834

FIG. 15

Score = 2481 (873.4 bits), Expect = 0.0, Sum P(2) = 0.0  
Identities = 469/474 (98%), Positives = 470/474 (99%), Frame = +1

Query: 1063 WVTGSSPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 1242  
+V PDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER  
Sbjct: 427 FVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 486

Query: 1243 LAEDTPPDEFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422  
LAEDTPPDEFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS  
Sbjct: 487 LAEDTPPDEFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query: 1423 PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSPYGLTPR 1602  
PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSPYGLTPR  
Sbjct: 547 PFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSPYGLTPR 606

Query: 1603 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTANLAA 1782  
GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTANLAA  
Sbjct: 607 GRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSSTANLAA 666

Query: 1783 VMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFPMHAHMRRHSAPTTP 1962  
VMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFPMHAHMRRHSAPTTP  
Sbjct: 667 VMVGDKTFEELSGIHDPKLHHPAQGFRTVWESSAEAYIKKSFPMHAHMRRHSAPTTP 726

Query: 1963 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN 2142  
RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN  
Sbjct: 727 RGVAMLTSDPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPAIEGYGIGLPQNSPLTSN 786

Query: 2143 LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRFAVTETLQMSIYHFAGLFVLLCLGLGSAL 2322  
LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRFAVTETLQMSIYHFAGLFVLLCLGLGSAL  
Sbjct: 787 LSEFISRYKSSGFIDLLHDKWYKMPVPCGKRFAVTETLQMSIYHFAGLFVLLCLGLGSAL 846

Query: 2323 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 2484  
LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP  
Sbjct: 847 LSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP 900

FIG. 16

Glutamate Receptor\_RAT\_AAD4165 MRRSLWVLSRCLLPDPCALVLA GVPSSSSHPPQPCQLKFGHVRGAGHLQPWTT  
Glutamate Receptor\_Human\_06039 MEFVRLWLG--LALALGP-----GS--AGGHPQPCGVRLARLGGSVRLGALLPR....  
21659259\_EXT2 MEFVRLWLG--LALALGP-----GS--AGGHPQPCGVRLARLGGSVRLGALLPR....

Glutamate Receptor\_RAT\_AAD4165 APRAASRAQEGGRAGAQRDD PESGTWRPPAP SQGARWLGSALHGSGPPGSRKLGEGAGAE  
Glutamate Receptor\_Human\_06039 APLARARA--RAALAR-----AALAPR-----  
21659259\_EXT2 APLARARA--RAALAR-----AALAPR-----

Glutamate Receptor\_RAT\_AAD4165 TLWPRDAL LFAVENLNRVEGL LFPYNLSLELVMAI EAGLGDPLMPFSSPS SPWSSDPFFSF  
Glutamate Receptor\_Human\_06039 -----LPHNLSLELVVAAPP-----ARDPASL  
21659259\_EXT2 -----LPHNLSLELVVAAPP-----ARDPASL

Glutamate Receptor\_RAT\_AAD4165 LQSCHTIVQGVSAALLAFPPQSGEMELDLSSSVLHIPVLSRHEF--PRESQPLFL  
Glutamate Receptor\_Human\_06039 TRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVL SLLREARAPLGAPNPFHL  
21659259\_EXT2 TRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVL SLLREARAPLGAPNPFHL

Glutamate Receptor\_RAT\_AAD4165 QLSLENSLSADAVIVSLIMNNWYNFSLLLCQEDWNITDFLLTENNSKFHLESVIN  
Glutamate Receptor\_Human\_06039 QLHWASPLETLLDVLVAVLQAHAWEDVGLAL CRTQDPGGVVALWTSRAG--RPPQLVLDLS  
21659259\_EXT2 QLHWASPLETLLDVLVAVLQAHAWEDVGLAL CRTQDPGGVVALWTSRAG--RPPQLVLDLS

Glutamate Receptor\_RAT\_AAD4165 ANLSTKDL LSLFQVQMDNR--NSTPIMVFCDDSDSIFQTFEMSTQFG--SPPELHWL  
Glutamate Receptor\_Human\_06039 RRD TGDAGLRARLAPMAAPVGGGEAPVPAAVLLGCDIARARRVLEA-----PPGPHWLL  
21659259\_EXT2 RRD TGDAGLRARLAPMAAPVGGGEAPVPAAVLLGCDIARARRVLEA-----VPPGPHWLL

Glutamate Receptor\_RAT\_AAD4165 GDSQNVEELETEGLPLGLAHUKITQSVFYYQDAELVARAATMQLLALLPST  
Glutamate Receptor\_Human\_06039 GTPLPPKALPTAGLPPGLLALGEVARPPLEAAIHDIVQLVARALGSAAGVQPKFALLPAP  
21659259\_EXT2 GTPLPPKALPTAGLPPGLLALGEVARPPLEAAIHDIVQLVARALGSAAGVQPKFALLPAP

Glutamate Receptor\_RAT\_AAD4165 NCMDKKTIN-LSSQLSRFLANTFRGLSGSKVKGSHISSENNFFVNQLQHPMK  
Glutamate Receptor\_Human\_06039 VNC GDLQPAGE SPGRFLARFLANT SFQGRTPGVWVT GSSQHMSKHFKAUSLRDDPRFA  
21659259\_EXT2 VNC GDLQPAGE SPGRFLARFLANT SFQGRTPGVWVT GSSQHMSKHFKAUSLRDDPRFA

Glutamate Receptor\_RAT\_AAD4165 PMVTRIGSWQGRVMSGIWPEQAQRHKTHFQHPNKLHVRVTL EHPFVETREVDDG  
Glutamate Receptor\_Human\_06039 EAWATIGSWRDGQD--PG--GASARPPPPQGAQVWPKLRVVTL EHPFVETREVDDG  
21659259\_EXT2 EAWATIGSWRDGQD--PG--GASARPPPPQGAQVWPKLRVVTL EHPFVETREVDDG

Glutamate Receptor\_RAT\_AAD4165 LCPAGQLCLDPMTNDSSMLDRLESSLHSSNDVP I KFKCCYGYCIDLLEQLAEDMNFDF  
Glutamate Receptor\_Human\_06039 QCPAGQLCLDPTND SATIDALFAALANG--SAPRALRCCYGYCIDLLERLAEDTPFDF  
21659259\_EXT2 QCPAGQLCLDPTND SATIDALFAALANG--SAPRALRCCYGYCIDLLERLAEDTPFDF

Glutamate Receptor\_RAT\_AAD4165 ELYVGDGKYGAWNGHWTLGLVGLDLSSTANMAVT SFSINSARSQVDFTSPEFFSTSLGI  
Glutamate Receptor\_Human\_06039 ELYVGDGKYGALRDGRWTGLVGLDLAGRAHMAVT SFSINSARSQVDFTSPEFFSTSLGI  
21659259\_EXT2 ELYVGDGKYGALRDGRWTGLVGLDLAGRAHMAVT SFSINSARSQVDFTSPEFFSTSLGI

Glutamate Receptor\_RAT\_AAD4165 EVRTRDTAARIGAFMWPLHWLWLGFLVALHTAFLTVIEWSPGCTTPGRNENKVS  
Glutamate Receptor\_Human\_06039 MVRARDTA SPIGAFMWPLHWSTWLG VFAALHTALFLTVIEWSPYGLTPRGNRSTVFS  
21659259\_EXT2 MVRARDTA SPIGAFMWPLHWSTWLG VFAALHTALFLTVIEWSPYGLTPRGNRSTVFS

Glutamate Receptor\_RAT\_AAD4165 SSALNLCYAILFGRTAAI EPPKCVTGFLMNLWAI FCFCLSYTANLA AAVVGDKTFE  
Glutamate Receptor\_Human\_06039 VSSALNLCYAILFRRTVSSKTPKCP TGRLLMNLWAI FCLLVLSSTANLA AAVVGDKTFE  
21659259\_EXT2 VSSALNLCYAILFRRTVSSKTPKCP TGRLLMNLWAI FCLLVLSSTANLA AAVVGDKTFE

Glutamate Receptor\_RAT\_AAD4165 ELSGIHD PKLHHP SQGFRFGTVRESSAEDVRSFPMEHYMRRYNVPATPDGVQYLKND  
Glutamate Receptor\_Human\_06039 ELSGIHD PKLHHPAQGFRFGTVWESSAEAYIKKSFPDMHAMRRHSAP TTPRGVAMLTSD  
21659259\_EXT2 ELSGIHD PKLHHPAQGFRFGTVWESSAEAYIKKSFPDMHAMRRHSAP TTPRGVAMLTSD

Glutamate Receptor\_RAT\_AAD4165 PEKLD AFIMDKALLDYEV SIDADCKLLTVGKPPAIEGYGIGLPPNSPLTSNISELISQW  
Glutamate Receptor\_Human\_06039 PPKLNAFIMDKSLLDYEV SIDADCKLLTVGKPPAIEGYGIGLPPNSPLTSNISEFISRYE  
21659259\_EXT2 PPKLNAFIMDKSLLDYEV SIDADCKLLTVGKPPAIEGYGIGLPPNSPLTSNISEFISRYE

Glutamate Receptor\_RAT\_AAD4165 SHGFIDLHDKWYKVP CGKRSFAVTETLQMGKHFSGLFVLLCIGFLSGLGEHIV  
Glutamate Receptor\_Human\_06039 SSGFIDLHDKWYKVP CGKRVFAVTETLQMSIYHFAGLFVLLCIGLGSALLSSLGEHAF  
21659259\_EXT2 SSGFIDLHDKWYKVP CGKRVFAVTETLQMSIYHFAGLFVLLCIGLGSALLSSLGEHAF

Glutamate Receptor\_RAT\_AAD4165 HRLLPRIKNSQLQYWLHTSQIHRALNTSFVEKQPKSKTKRVEKSRWRRWTCKTEGD  
Glutamate Receptor\_Human\_06039 FRLALPRIKGSRLQYWLHTSQIHRALNTEPDEGS--KEETAEEAPR-----GP..  
21659259\_EXT2 FRLALPRIKGSRLQYWLHTSQIHRALNTEPDEGS--KEETAEEAPR-----GP..

Glutamate Receptor\_RAT\_AAD4165 SEELSFPRSLGPPQLMVNTSNLSHNDQRYIEND EEQNQLGTQAHQD IPLPQRREL  
Glutamate Receptor\_Human\_06039 -----EEQQQQQQDQPTAPEGVKRRARRAVDKERVRFLLEP VVVVAPEADAEAEAAE--REG  
21659259\_EXT2 -----EEQQQQQQDQPTAPEGVKRRARRAVDKERVRFLLEP VVVVAPEADAEAEAAE--REG

Glutamate Receptor\_RAT\_AAD4165 PASLTNGEADS LNVTRSSVI QELSELDEQI QI RQELQLASRR--TEEEYQKNCTCE  
Glutamate Receptor\_Human\_06039 PVWLCSYGPAPARPFGAPQPGELQELERTEARERERLROAVRREGQLAQLGDSAEHRP  
21659259\_EXT2 PVWLCSYGPAPARPFGAPQPGELQELERTEARERERLROAVRREGQLAQLGDSAEHRP

Glutamate Receptor\_RAT\_AAD4165 S-----  
Glutamate Receptor\_Human\_06039 RRL LQARAAPAEAPPHSGRPGSQE  
21659259\_EXT2 RRL LQARAAPAEAPPHSGRPGSQE

FIG. 17

ATGGAGTTTGTGCGGGCGCTGTGGCTGGGCCTGGCGCTGGCGCTGGGGCCGGGGTCCGCGGGGGG  
 CACCCTCAGCCGTGCGGCGTCTGGCGCGCTCGGGGGCTCCGTGCGCTGGGCGCCCTCCTGCCCC  
 GCGCGCTCTCGCCCGCGCCCGCGCCCGCGCCCTGGCCCGGGCCGCGCTGGCGCCGCGGCTGCC  
 GCACAACCTGAGCTTGGAGCTGGTGGTCCGCGCGCCCCCGCCCGCGACCCCGCCTCGCTGACCCGC  
 GGCCTGTGCCAGGCGCTGGTGCCTCCGGGCGTGGCGGCCCTGCTCGCCTTCCCGAGGCTCGGCCCC  
 AGCTGCTGCAGCTGCACTTCTGGCGCGGCCACCGAGACCCCGTGTCTCAGCCTGCTGCGGCGGG  
 AGGCGCGCGCGCCCTCGGAGCCCCGAACCCATTCCACCTGCAGCTGCACTGGGCCAGCCCCCTGG  
 AGACGCTGCTGGATGTGCTGGTGGCGGTGCTGCAGGCGCACGCTGGGAAGACGTGCGCCTGGCCC  
 TGTGCCGCACTCAGGACCCCGCGGCGCTGGTGGCCCTCTGGACAAGCCGGGCTGGCCGGCCCCAC  
 AGCTGGTCTTGACCTAAGCCGGCGGGACACGGGAGATGCAGGACTGCGGGACAGCCTGGCCCCGA  
 TGGCGGCGCCAGTGGGGGTGAAGCACCGGTACCCGCGGCGGTCTCTCGGCTGTGACATCGCCC  
 GTGCCCCGTGCGGTGCTGGAGGCGGTACCTCCCGGCCCGCACTGGCTGTTGGGGACACCACTGCCGCC  
 CAAGGCCCTGCCACCGCGGGGCTGCCACCAGGGCTGCTGGCGCTGGGCGAGGTGGCACGACCCCC  
 GCTGGAGGCCGCCATCCATGACATTGTGCAACTGGTGGCCCGGGCGCTGGGCAGTGGCGGCCAGGT  
 GCAGCCGAAGCGAGCCCTCCTCCCCGCCCGGTCAACTGCGGGGACCTGCAGCCGGCCGGGCCCGA  
 GTCCCCGGGGCGCTTCTTGACACGGTTCCTGGCCAACACGTCTTCCAGGGCCGACGGGCCCGGTG  
 TGGGTGACAGGCACTCCAGGTACACATGTCTCGGCACCTTAAGGTGTGGAGCCTTCGCCGGGACC  
 CACGGGGCGCCCCGGCCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAACGGG  
 GAGGTGCCTCTGCACGGCCCCCGCCCCACAGGGTGGCCAGGTCTGGCCCAAGCTGCGTGTGGTAA  
 CGCTGTTGGAACACCCATTTGTGTTTGGCCGTGATCCAGACGAAGACGGGCACTGCCAGCGGGGC  
 AGCTGTGCCTGGACCTGGCACCAACGACTCGGCCACCTGGACGCACTGTTCCCGCGCTGGCCAA  
 CGGCTCAGCGCCCCGTGCCCTGCGCAAGTGTGCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTG  
 GCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGG  
 GACGGCCGCTGGACCGGCCCTGGTGGGGACCTGCTGGCCGGCCGGGCCACATGGCGGTACCCAGC  
 TTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACCAGCCCCCTTCTCTCCACCAGCCTGG  
 GCATCATGGTGGGGACAGGGACACGGCCTCACCCATCGGTGCCCTTATGTGGCCCTGCACTGGTC  
 CACGTGGCTGGGCGTCTTTGCGGCCCTGCACCTCACCGCGCTCTTCTCACCCTGTACGAGTGGCGT  
 AGCCCCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCTACTCCTCAGCCCTCA  
 ACCTGTGCTACGCCATCCTCTTCAGACGCAACCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCCG  
 CCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGTGCTCCAGCTACACGGCCAACCTGGCT  
 GCCGTGCTGGTGGGGACAAGACCTTCGAGGAGCTGTGGGGATCCACGACCCCAAGCTGCACCAC  
 CCGGCGCAGGGCTTCCGCTTCGGCACCGTGTGGGAGAGCAGCGCCGAGGCGTACATCAAGAAGAGC  
 TTCCCCGACATGCACGCACACATGCGGCGCCACAGCGCGCCACCAACGCCCGCGGGCGTCCCATG  
 CTCACGAGCGACCCCCCAAGCTCAACGCCTTCATCATGGACAAGTCGCTCCTGGACTACGAGGTCT  
 CCATCGACGCCGACTGCAAACTGCTGACCGTGGGAAAGCCCTTCGCCATTGAGGGCTATGGGATCG  
 GACTGCCCCAGAACTCGCCGCTCACCTCCAACCTGTCCGAGTTCATCAGCCGCTACAAAGTCTCCGG  
 CTTATCGACCTGCTCCACGACAAGTGGTACAAGATGGTGCCTTGGCGCAAGCGGGTCTTTGCGGTT  
 ACAGAGACCCTGCAGATGAGCATCTACCACTTCGCGGGCCTCTTCGTGTTGCTGTGCCTGGGCCTGG  
 GCAGCGCTCTGCTCAGCTCGCTGGGCGAGCACGCCTTCTTCGGCCTGGCGCTGCCGCGCATCCGCA  
 GGGGAGCAGGCTGCAGTACTGGCTGCACACCAGCCAGAAATCCACCGCGCCCTCAACACGGAGCC  
 ACCAGAGGGGTGGAAGGAGGAGACGGCAGAGGCGGAGCCAGCGGCCCGGAGGTGGAGCAGCAGC  
 AGCAGCAGCAGGACCAGCCAACGGCTCCGGAGGGCTGGAAACGGGGCGCGCCGGGGCGGTGGACAAG  
 GAGCGCCGCGTGCCTTCTGCTGGAGCCCGCGGTGGTTGTGGCACCCGAAGCGGACGCGGAGGCG  
 GAGGCTGCGCCGCGAGAGGGCCCCGTCTGGCTGTGCTCCTACGGCCGCCCGCCCGCCGCAAGGCC  
 ACGGGGGCCCCCAGCCCGGGGAGCTGCAGGAGCTGGAGCGCCGATCGAAGTCGCGCGTGAAGCG  
 GCTCCGCCAGGCCCTGGTGGCGCGCGGCCAGCTCCTGGCACAGCTCGGGGACAGCGCACGTCACCG  
 GCCTCGGCGCTGCTTCAGGCCAGAGCGGCCCGCGGAGGCCCCACCACTCTGGCCGACCGGG  
 GAGCCAGGAATGA



FIG. 18

MEFVRALWLGLALALGPGSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARAALAPRLPH  
NLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAPPEARPELLQLHFLAAATETPVLSLLRREARAP  
LGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTCQDPGGLVALWTSRAGRPPQLVLDLS  
RRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLP  
PGLLALGEVARPPLEAAIHDIQVLVARALGSAAQVQPKRALLPAPVNCGLQAPGPESPGRFLARFLANT  
SFQGRTPGVWVTGSSQVHMSRHFVWVSLRRDPRGAPAWATVGSWRDGGQLDLEPGGASARPPPPQGAQ  
VWPKLRVVTLLHHPFVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYCI  
DLLERLAEDTPFDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSSENSARSQVVDFTSPFFS  
TSLGIMVRARDTASPIGAFMWPLHWSTWLGVFALHLTALFLTVYEWRSPLYGLTPRGRNRSTVFSYSSA  
LNL CYAILFRRTVSSKTPKCPTGRLLMNLWAFCLLVLSY TANLAAVMVGDKTFFELSGIHDPKLHHPA  
QGFRFGTVWESSAEA YIKKSFPDMHAHMRRHSAPTTPRGVAMLTSDPPKLNAFIMDKSLLDYEVSIDAD  
CKLLTVGKPFATIEGYGIGLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMPVPCGKR VFAVTETLQMSIY  
HFAGLFVLLCLGLGSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEEAP  
SGPEVEQQQQQQDQPTAPEGWKRRARRAVDKERRVRFLEPAVVVAPEADAEAEAAPREGPVWLCSYG  
RPPAARPTGAPQPGELQELERRIEVARERLRQALVRRGQLLAQLGDSARHRPRRLQARAAPAEAPPHSG  
RPGSQE

FIG. 19

Score = 5188 (778.4 bits), Expect = 0.0, Sum P(4) = 0.0

Identities = 1068/1092 (97%), Positives = 1068/1092 (97%), Strand = Plus / Plus

Query: 1019 GGTTCCTGGCCAACACGTCCTTCCAGGGCCGCACGGGCCCCGTGTGGGTGACAGGCAGCT 1078  
GGTTCCTGGCCAACACGTCCTTCCAGGGCCGCACGGGCCCCGTGTGGGTGACAGGCAGCT

Sbjct: 22747 GGTTCCTGGCCAACACGTCCTTCCAGGGCCGCACGGGCCCCGTGTGGGTGACAGGCAGCT 22806

Query: 1079 CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG 1138  
CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG

Sbjct: 22807 CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG 22866

Query: 1139 CCCCCGGCCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAAACGGGGAG 1198  
CCCCGGCCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAAACGGGGAG

Sbjct: 22867 CCCCCGGCCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGGAAACGGGGAG 22926

Query: 1199 GTGCCTCTGCACGGCCCCCGCCCCACAGGGTGCCAGGTCTGGCCCAAGCTGCGTGTGG 1258  
GTGCCTCTGCACGGCCCCCGCCCCACAGGGTGCCAGGTCTGGCCCAAGCTGCGTGTGG

Sbjct: 22927 GTGCCTCTGCACGGCCCCCGCCCCACAGGGTGCCAGGTCTGGCCCAAGCTGCGTGTGG 22986

Query: 1259 TAACGCTGTTGGAACACCCATTTGTGTTTGCCCGTGATCCAGACGAAGACGGGCAGTGCC 1318  
TAACGCTGTTGGAACACCCATTTGTGTTTGCCCGTGATCCAGACGAAGACGGGCAGTGCC

Sbjct: 22987 TAACGCTGTTGGAACACCCATTTGTGTTTGCCCGTGATCCAGACGAAGACGGGCAGTGCC 23046

Query: 1319 CAGCGGGGCAGCTGTGCCTGGACCCTGGCACCAACGACTCGGCCACCCTGGAACGCACTGT 1378  
CAGCGGGGCAGCTGTGCCTGGACCCTGGCACCAACGACTCGGCCACCCTGGAACGCACTGT

Sbjct: 23047 CAGCGGGGCAGCTGTGCCTGGACCCTGGCACCAACGACTCGGCCACCCTGGAACGCACTGT 23106

Query: 1379 TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT 1438  
TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT

Sbjct: 23107 TCGCCGCGCTGGCCAACGGCTCAGCGCCCCGTGCCCTGCGCAAGTGCTGCTACGGCTACT 23166

# FIG. 19 Continued

Query: 1439 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 1498  
 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG  
 Sbjct: 23167 GCATTGACCTGCTGGAGCGGCTGGCGGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 23226

Query: 1499 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCCCTGGTCGGGGACC 1558  
 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCCCTGGTCGGGGACC  
 Sbjct: 23227 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCGCTGGACCGGCCCTGGTCGGGGACC 23286

Query: 1559 TGCTGGCCGGCCGGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC 1618  
 TGCTGGCCGGCCGGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC  
 Sbjct: 23287 TGCTGGCCGGCCGGGCCACATGGCGGTACACAGCTTCAGTATCAACTCCGCCCGCTCAC 23346

Query: 1619 AGGTGGTGGACTTCACAGCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGGGGAC 1678  
 AGGTGGTGGACTTCACAGCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGGGGAC  
 Sbjct: 23347 AGGTGGTGGACTTCACAGCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGGGGAC 23406

Query: 1679 GGGACACGGCCTCACCCATCGGTGCCTTTATGTGGCCCTGCACTGGTCCACGTGGCTGG 1738  
 GGGACACGGCCTCACCCATCGGTGCCTTTATGTGGCCCTGCACTGGTCCACGTGGCTGG  
 Sbjct: 23407 GGGACACGGCCTCACCCATCGGTGCCTTTATGTGGCCCTGCACTGGTCCACGTGGCTGG 23466

Query: 1739 GCGTCTTTGCGGCCCTGCACCTCACCGCGCTCTTCCTCACCGGTACGAGTGGCGTAGCC 1798  
 GCGTCTTTGCGGCCCTGCACCTCACCGCGCTCTTCCTCACCGGTACGAGTGGCGTAGCC  
 Sbjct: 23467 GCGTCTTTGCGGCCCTGCACCTCACCGCGCTCTTCCTCACCGGTACGAGTGGCGTAGCC 23526

Query: 1799 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCCTACTCCTCAGCCC 1858  
 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCCTACTCCTCAGCCC  
 Sbjct: 23527 CCTACGGCCTCACGCCACGTGGCCGCAACCGCAGCACCGTCTTCTCCTACTCCTCAGCCC 23586

Query: 1859 TCAACCTGTGCTACGCCATCCTCTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC 1918  
 TCAACCTGTGCTACGCCATCCTCTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC  
 Sbjct: 23587 TCAACCTGTGCTACGCCATCCTCTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC 23646

Query: 1919 CCACGGGCCGCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGCTGTCCAGCT 1978  
 CCACGGGCCGCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGCTGTCCAGCT  
 Sbjct: 23647 CCACGGGCCGCTGCTCATGAACCTCTGGGCCATCTTCTGCCTGCTGGTGCTGTCCAGCT 23706

Query: 1979 ACACGGCCAACCTGGCTGCCGTATGGTCGGGGACAAGACCTTCGAGGAGCTGTGGGGGA 2038  
 ACACGGCCAACCTGGCTGCCGTATGGTCGGGGACAAGACCTTCGAGGAGCTGTGGGGGA  
 Sbjct: 23707 ACACGGCCAACCTGGCTGCCGTATGGTCGGGGACAAGACCTTCGAGGAGCTGTGGGGGA 23766

Query: 2039 TCCACGACCCCAAGCTGCACCACC-CGGCGCAGGGCTTCCGCTTCGGCACCCTGTGGGAG 2097  
 TCCACGACCCCAAG TG C CC CGG G GGGCT C G T GGC G G GGG  
 Sbjct: 23767 TCCACGACCCCAAGGTGGGCGGCTCGG-G--GGGCTGCGGGT--GGCCTTGGG-GGGCT 23820

Query: 2098 AGCAGCG-CCGAGG 2110  
 AGC G G CC GG  
 Sbjct: 23821 AGCGGTGGCCCCGG 23834

FIG. 20

Score = 4730 (1665.0 bits), Expect = 0.0, P = 0.0

Identities = 900/900 (100%), Positives = 900/900 (100%), Frame = +1

Query: 1 MEFVRALWLGLALALGPSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARA 180  
MEFVRALWLGLALALGPSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARA  
Sbjct: 1 MEFVRALWLGLALALGPSAGGHPQPCGVLARLGGSVRLGALLPRAPLARARARAALARA 60

Query: 181 ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLA 360  
ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLA  
Sbjct: 61 ALAPRLPHNLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLHFLA 120

Query: 361 AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR 540  
AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR  
Sbjct: 121 AATETPVLSLLRREARAPLGAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCR 180

Query: 541 TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC 720  
TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC  
Sbjct: 181 TQDPGGLVALWTSRAGRPPQLVLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLGC 240

Query: 721 DIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLPPGLLALGEVARPPLEAAIHNDIVQLV 900  
DIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLPPGLLALGEVARPPLEAAIHNDIVQLV  
Sbjct: 241 DIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLPPGLLALGEVARPPLEAAIHNDIVQLV 300

Query: 901 ARALGSAAQVQPKRALLPAPVNCGLDQAGPESPGRFLARFLANTSFOGRTGPVWVTGSS 1080  
ARALGSAAQVQPKRALLPAPVNCGLDQAGPESPGRFLARFLANTSFOGRTGPVWVTGSS  
Sbjct: 301 ARALGSAAQVQPKRALLPAPVNCGLDQAGPESPGRFLARFLANTSFOGRTGPVWVTGSS 360

Query: 1081 QVHMSRHFVWVSLRRDPRGAPAWATVGSWRDQQLDLEPGGASARPPPPQGAQVWPCLRVRV 1260  
QVHMSRHFVWVSLRRDPRGAPAWATVGSWRDQQLDLEPGGASARPPPPQGAQVWPCLRVRV  
Sbjct: 361 QVHMSRHFVWVSLRRDPRGAPAWATVGSWRDQQLDLEPGGASARPPPPQGAQVWPCLRVRV 420

Query: 1261 TLLEHPFVFARDPDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC 1440  
TLLEHPFVFARDPDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC  
Sbjct: 421 TLLEHPFVFARDPDEDGQCAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCYGYC 480

Query: 1441 IDLLERLAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ 1620  
IDLLERLAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ  
Sbjct: 481 IDLLERLAEDTPFDFFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ 540

# FIG. 20 Continued

Query: 1621 VVDFTSPFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSP 1800  
VVDFTSPFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSP  
Sbjct: 541 VVDFTSPFFSTSLGIMVRARDTASPIGAFMWPLHWSTWLGVFAALHLTALFLTVEYWRSP 600

Query: 1801 YGLTPRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY 1980  
YGLTPRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY  
Sbjct: 601 YGLTPRGRNRSTVFSYSSALNLCYAILFRRTVSSKTPKCPTGRLLMNLWAI FCLLVLSY 660

Query: 1981 TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRFGTVWESSAEAYIKKSFPMHAHMRRH 2160  
TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRFGTVWESSAEAYIKKSFPMHAHMRRH  
Sbjct: 661 TANLAAMVGDKTFEELSGIHDPKLHHPAQGFRFGTVWESSAEAYIKKSFPMHAHMRRH 720

Query: 2161 SAPTTPRGVAML/TS DPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPFAIEGYGIGLPQN 2340  
SAPTTPRGVAML/TS DPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPFAIEGYGIGLPQN  
Sbjct: 721 SAPTTPRGVAML/TS DPPKLNAFIMDKSLLDYEVSIDADCKLLTVGKPPFAIEGYGIGLPQN 780

Query: 2341 SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKR VFAVTETLQMSIYHFAGLFVLLCL 2520  
SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKR VFAVTETLQMSIYHFAGLFVLLCL  
Sbjct: 781 SPLTSNLSEFISRYKSSGFIDLLHDKWYKMVPCGKR VFAVTETLQMSIYHFAGLFVLLCL 840

Query: 2521 GLGSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEAEF 2700  
GLGSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEAEF  
Sbjct: 841 GLGSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEETAEAEF 900

FIG. 21

Glutamate_Receptor_RAT_AAD4165	MRRSLWVLSRCLLPFP CALVLA	GVPSSSHPPQPCQLKFGHAFVGAHLQPWTT
Glutamate_Receptor_Human_06039	MEFVRALWLG--LALALGP-----	GS--AGCHPQPCGV LARLGGSVRLGALLPE----
21659259_EXT3	MEFVRALWLG--LALALGP-----	GS--AGCHPQPCGV LARLGGSVRLGALLPE----
Glutamate_Receptor_RAT_AAD4165	APRAASRAQEGGRAGAQRDDPESGTWRPPAP	SQGARWLGSALHGGPPGSRKLGEAGAGAE
Glutamate_Receptor_Human_06039	APLARARA-----RAALAR-----	AALAPR-----
21659259_EXT3	APLARARA-----RAALAR-----	AALAPR-----
Glutamate_Receptor_RAT_AAD4165	TLWPRDALLFAVENLNRVEGL	LFYNLSELVVAI EAGLGDLPLMPFSSPSPWSSDFEF
Glutamate_Receptor_Human_06039	-----	LPHNLSELVVAAPP-----ARDPASL
21659259_EXT3	-----	LPHNLSELVVAAPP-----ARDPASL
Glutamate_Receptor_RAT_AAD4165	LQSCHTGVQGVSAALLAFPPSQSGEMDEL	SSVLHIPVLSRHEF--PRESQNLHL
Glutamate_Receptor_Human_06039	TRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVL	SLLRREARAPLGAPNPFHL
21659259_EXT3	TRGLCQALVPPGVAALLAFPEARPELLQLHFLAAATETPVL	SLLRREARAPLGAPNPFHL
Glutamate_Receptor_RAT_AAD4165	QLSLENSLSADAVTVSLTMNNWYNFSLL	COEDWNI TDFLLTENNSKFHLESVIN
Glutamate_Receptor_Human_06039	QLHWASPL ETLLDVLVAVLQAHAWEDVGLALCRT	QDPGGGLVALWTSRAG-RPPQLVLDLS
21659259_EXT3	QLHWASPL ETLLDVLVAVLQAHAWEDVGLALCRT	QDPGGGLVALWTSRAG-RPPQLVLDLS
Glutamate_Receptor_RAT_AAD4165	ANLSTKD LLSFLQVQMDNRR--NSTPTMVF	GCDDSDSIRQFEMSTQFGSPPELHWL
Glutamate_Receptor_Human_06039	RRDTGDAGLRLARLAPMAAPVGG EAPVPAAVLLGCD	IARARRVLEA-----PPGPHVLL
21659259_EXT3	RRDTGDAGLRLARLAPMAAPVGG EAPVPAAVLLGCD	IARARRVLEA-----VPPGPHVLL
Glutamate_Receptor_RAT_AAD4165	GDSONVEELRTEGLPLGLAHGKTIQSVFYYQDA	ELVARATATMQPELALLPST
Glutamate_Receptor_Human_06039	GTPLPPKALPTAGLPFGLLALGEVARDPLEAAIHD	IVQLVARALGSAAQVQPKRALLPAP
21659259_EXT3	GTPLPPKALPTAGLPFGLLALGEVARDPLEAAIHD	IVQLVARALGSAAQVQPKRALLPAP
Glutamate_Receptor_RAT_AAD4165	MNCMDKKT TN-LSSQQLSFLANTFRGLGS	KVKSSISSENFFWNLOHDPMEK
Glutamate_Receptor_Human_06039	VNCGDLQPAQPE SPGRFLARFLANTSFQGR	GPVWVTGSSQVHMSRHF KWWSLRDPDGA
21659259_EXT3	VNCGDLQPAQPE SPGRFLARFLANTSFQGR	GPVWVTGSSQVHMSRHF KWWSLRDPDGA
Glutamate_Receptor_RAT_AAD4165	PLWVTRGSGWQGRVDSGIWPEQAQHKTHFOH	PKNLHLRVVTLLEHPFVFTEFVDEG
Glutamate_Receptor_Human_06039	PAWATVGSWFDGQLDLEPG--GASARPPPP	QGAQVWP KLRVVTLEHPFVFARDPDEDG
21659259_EXT3	PAWATVGSWFDGQLDLEPG--GASARPPPP	QGAQVWP KLRVVTLEHPFVFARDPDEDG
Glutamate_Receptor_RAT_AAD4165	LCPAGQLCLDPMTNDSSMLDRLFS SLHSSND	VPIKFKCCYGYCIDLLEQLAEDMNFDF
Glutamate_Receptor_Human_06039	QCPAGQLCLDPGTND SATLDALFAALANG--	SAPRALRKCCYGYCIDLLERLAEDTPFDF
21659259_EXT3	QCPAGQLCLDPGTND SATLDALFAALANG--	SAPRALRKCCYGYCIDLLERLAEDTPFDF
Glutamate_Receptor_RAT_AAD4165	ELYLVGDGKYGAWNGHWTGLVGDLLS	TANMAVTSFINSARSQVDFTSFFSTSLGI
Glutamate_Receptor_Human_06039	ELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAV	TSFINSARSQVDFTSFFSTSLGI
21659259_EXT3	ELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAV	TSFINSARSQVDFTSFFSTSLGI

FIG. 22

21659259_EXT_3	MEFVRALWGLLALGPGSAGGH	PQPCGV	LARLGGSVRLGALLPRAPLARARARAALARA
21659259_EXT_2	MEFVRALWGLLALGPGSAGGH	PQPCGV	LARLGGSVRLGALLPRAPLARARARAALARA
21659259_EXT_1	MEFVRALWGLLALGPGSAGGH	PQPCGV	LARLGGSVRLGALLPRAPLARARARAALARA
21659259_EXT_3	ALAPRLPHNLSLELVVAAP	PARDPAST	TRGLCQALVPPGVAALLAFPEARPELQLHFLA
21659259_EXT_2	ALAPRLPHNLSLELVVAAP	PARDPAST	TRGLCQALVPPGVAALLAFPEARPELQLHFLA
21659259_EXT_1	ALAPRLPHNLSLELVVAAP	PARDPAST	TRGLCQALVPPGVAALLAFPEARPELQLHFLA
21659259_EXT_3	AATEPVLSSLRREARAP	LGAPNPFHLQLH	WASPLETLIDVLVAVLQAHAWEDVGLALCR
21659259_EXT_2	AATEPVLSSLRREARAP	LGAPNPFHLQLH	WASPLETLIDVLVAVLQAHAWEDVGLALCR
21659259_EXT_1	AATEPVLSSLRREARAP	LGAPNPFHLQLH	WASPLETLIDVLVAVLQAHAWEDVGLALCR
21659259_EXT_3	TQDPGGLVALWTSRAGR	PQVLVLDLS	RDGTGDAGLRARLAPMAAPVGGEPVPAAVLLGC
21659259_EXT_2	TQDPGGLVALWTSRAGR	PQVLVLDLS	RDGTGDAGLRARLAPMAAPVGGEPVPAAVLLGC
21659259_EXT_1	TQDPGGLVALWTSRAGR	PQVLVLDLS	RDGTGDAGLRARLAPMAAPVGGEPVPAAVLLGC
21659259_EXT_3	DIARARRVLEAVPPGP	HWLLGTPLP	PKALPTAGLPPGLLALGEVARPPEAAIHDIVOLV
21659259_EXT_2	DIARARRVLEAVPPGP	HWLLGTPLP	PKALPTAGLPPGLLALGEVARPPEAAIHDIVOLV
21659259_EXT_1	DIARARRVLEAVPPGP	HWLLGTPLP	PKALPTAGLPPGLLALGEVARPPEAAIHDIVOLV
21659259_EXT_3	ARALGSAAQVQPKRAL	LPAVNC	GDLQPAGPESPGRLARFLANTSFOGRTGPVWVTGSS
21659259_EXT_2	ARALGSAAQVQPKRAL	LPAVNC	GDLQPAGPESPGRLARFLANTSFOGRTGPVWVTGSS
21659259_EXT_1	ARALGSAAQVQPKRAL	LPAVNC	GDLQPAGPESPGRLARFLANTSFOGRTGPVWVTGSS
21659259_EXT_3	QVHMSRHF	KVWSLRDP	RGAFAWATVGSWRDQLDLEPGGASARPP
21659259_EXT_2	QVHMSRHF	KVWSLRDP	RGAFAWATVGSWRDQLDLEPGGASARPP
21659259_EXT_1	QVHMSRHF	KVWSLRDP	RGAFAWATVGSWRDQLDLEPGGASARPP
21659259_EXT_3	TLLEHPFVFARD	PDEBDGQCP	AGQLCLDPGTNDSATLDAALFALANGSAPRALRKC
21659259_EXT_2	TLLEHPFVFARD	PDEBDGQCP	AGQLCLDPGTNDSATLDAALFALANGSAPRALRKC
21659259_EXT_1	TLLEHPFVFARD	PDEBDGQCP	AGQLCLDPGTNDSATLDAALFALANGSAPRALRKC

## FIG. 22 Continued

21659259_EXT_3	RLLQARAAPAEAPPHSGRPGSQE
21659259_EXT_2	RLLQARAAPAEAPPHSGRPGSQE
21659259_EXT_1	RLLQARAAPAEAPPHSGRPGSQE



FIG. 23

ACGCGTTACTCCTACCAGGTTGTAGCATGCATCTTTTTGAGAGAGCAGCTGGGATCGAGTA  
TACTCTTGACTTAAATATGTTTGTTTATAAAGACAAATGGAGAAATCAATTTTTTCCCTGA  
ATTCTTAGGAGCACTTTAGTGAATAAAGAACCTGACAGTATGCTGGCCACATGTTTAAGG  
ACAAAGGTGTCTGGGGAAATAAGCAAGATCATAGAGGAGCTTTCCTAATTGACCGAAGTCC  
TGAGTACTTCGAACCCATTTTGAACACTTGCCTCATGGACAGCTCATTGTAAATGATGGCA  
TTAATTTATTGGGTGTGTTAGAAGAAGCAAGATTTTTTGGTATTGACTCATTGATTGAACAC  
CTAGAAGTGGCAATAAAGAATTCTCAACCACCGGAGGATCATTACCAATATCCCGAAAGG  
AATTTGTCCGATTTTTTGCTAGCAACTCCAACCAAGTCAGAACTGCGATGCCAGGGTTTGAA  
CTTCAGTGGTGCTGATCTTCTCGTTTGGACCTTCGATACATTAACCTCAAAATGGCCAATT  
TAAGCCGCTGTAATCTTGACATGCAAATCTTTGCTGTGCAAATCTTGAACGAGCTGATCTC  
TCTGGATCAGTGCTTGACTGTGCGAATCTCCAGGGAGTCAAGATGCTCTGTTCTAATGCAG  
AAGGAGCATCCCTGAAACTGTGTAATTTTGAGGATCCTTCTGGTCTTAAAGCCAATTTAGA  
AGGTGCTAATCTGAAAGGTGTGGATATGGAAGGAAGTCAGATGACAGGAATTAACCTGAG  
AGTGGCTACCTTAAAAAATGCAAAGTTGAAGAACTGTAACTCAGAGGAGCAACTCTGGC  
AGGAACTGATTTAGAGAATTGTGATCTGTCTGGGTGTGATCTTCAAGAAGCCAACCTGAGA  
GGGTCCAACGTGAAGGGAGCTATATTTGAAGAGATGCTGACACCACTACACATGTCACAAA  
GTGTCAGATGAGAATTTTAGGGGCTGGAGGAAGATGTAAAAGATGAAAATGTTTTCTTAT  
CACTTTTCTTTCTCCACCCACTCAGTTGTCTAGAAGAAATAACACTGTAAGGAAATTTAAAA  
AAAAAAA

**FIG. 24**

MLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGINLLGVLEEARFFGID  
SLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGLNFSGADLSRLDLRYINFKMAN  
LSRCNLAHANLCCANLERADLSGSVLD CANLQGVKMLCSNAEGASLKLCNFEDPSGLKANLE  
GANLKGVDMEGSQMTGINLRVATLKN AKLKNCNLRGATLAGTDLENCDSLGC DLQEANLRGS  
NVKGAIFEEMLTPLHMSQSVR

## FIG. 25

Score = 1486 (523.1 bits), Expect = 1.4e-151, P = 1.4e-151

**Identities = 286/286 (100%), Positives = 286/286 (100%), Frame = +1**

Query: 130 RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI 309  
RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI  
Sbjct: 104 RSTLVNKEPDSMLAHMFKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGI 163

Query: 310 NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGL 489  
NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGL  
Sbjct: 164 NLLGVLEEARFFGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGL 223

Query: 490 NFSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGSVLD CANLQGVKMLCS 669  
NFSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGSVLD CANLQGVKMLCS  
Sbjct: 224 NFSGADLSRLDLRYINFKMANLSRCNLAHANLCCANLERADLSGSVLD CANLQGVKMLCS 283

Query: 670 NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKN AKLKNCNL RGA 849  
NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKN AKLKNCNL RGA  
Sbjct: 284 NAEGASLKL CNFEDPSGLKANLEGANLKGVDMEGSQMTGINLRVATLKN AKLKNCNL RGA 343

Query: 850 TLAGTDLENCDSL GCDLQ EANLRG SNVKG AIF EEMLTPLHMSQSV R 987  
TLAGTDLENCDSL GCDLQ EANLRG SNVKG AIF EEMLTPLHMSQSV R  
Sbjct: 344 TLAGTDLENCDSL GCDLQ EANLRG SNVKG AIF EEMLTPLHMSQSV R 389

FIG. 26

TTTCCAGGGTTCTAGCCTGTTTCATCTAGCCCC**ATG**ATGGCTGTGGACATCGAGTACAGATACAACCTGCAT  
GGCTCCTTCCTTGCGCCAAGAGAGGTTTGCCTTTAAGATCTCACCAAAGCCCAGCAAACCACTGAGGCCT  
TGTATTCAGCTGAGCAGCAAGAATGAAGCCAGTGAATGGTGGCCCCGGCTGTCCAGGAGAAGAAGGTGA  
AAAAGCGGGTGTCTTTCGAGACAACCAGGGGCTGGCCCTGACAATGGTCAAAGTGTCTCGGAATTCGA  
TGACCCGCTAGATATGCCATTCAACATCACCGAGCTCCTAGACAACATTGTGAGCTTGACGACAGCAGAG  
AGCGAGAGCTTTGTTCTGGATTTTTCCAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGG  
CCGACCACGTCTGCCTTGAGAACTGTGTGCTCAAGGACAAGGCCATTGCAGGCACTGTGAAGGTTTCAGAA  
CCTCGCATTTGAGAAGACCGTGAAAATAAGGATGACGTTTCGACACCTGGAAGAGCTACACAGACTTTCCT  
TGTCAGTACGTGAAGGACACTTATGCCGGTTCAGACAGGGACACGTTCTCCTTCGACATCAGCTTGCCCG  
AGAAGATTCACTCTTATGAAAGAATGGAGTTTGCTGTGTACTACGAGTGCAATGGACAGACGTACTGGGA  
CAGCAACAGAGGCAAGAAGTATAGGATCATCCGGGCTGAGTTAAAATCTACCCAGGGAATGACCAAGCCC  
CACAGTGGACCGGATTTGGGAATATCCTTTGACCAGTTCGGAAGCCCTCGGTGTTCTTATGGTCTGTTTC  
CAGAGTGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTAC**TAG**TGACTGCAGGTGACAGGGCG  
TGGCGGAGCTGCCACA

FIG. 27

MMAVDIEYRYNCMAPSLRQERFAFKISPKPSKPLRPCIQLSSKNEASGMVAPAVQEKKVKKRVSFADNQG  
LALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESESFVLDFSQPSADYLDFRNRLQADHVCLENCVL  
KDKAIAAGTVKVQNLAFKTVKIRMTFTWKSYSYTDFFCQYVKDTYAGSDRDTFSFDISLPEKIQSYERMEF  
AVYYECNGQTYWDSNRGKNYRIIRAELKSTQGMTKPHSGPDLGISFDQFGSPRCSYGLFPEWPSYLGYEK  
LGPYY

FIG. 28

Score = 3195 (479.4 bits), Expect = 2.8e-138, P = 2.8e-138  
Identities = 763/903 (84%), Positives = 763/903 (84%), Strand = Plus / Plus

Query: 6 AGGGTTCTAGCCTGTTTCATCTAGCCCCATGATGGCTGTGGACATCGAGTACAGATACAAC 65  
AG TTCTAGCCTG C TCTA C TGATGGC GTGGACAT GA TACAG TACA C  
Sbjct: 65 AGACTTCTAGCCTGCCCTCTAACG---TGATGGCCGTGGACATAGAATACAGCTACAGC 121

Query: 66 TGCATGGCTCCTTCCTTGCGCCAAGAGAGGTTTGCCTTTAAGATCTCACAAAGCCCAGC 125  
G ATGC CTTT TCGC AGAG G TT CCTT AAGATCTC CC AA C A C  
Sbjct: 122 AGTATGGCCCTTCTCTGCGCAGAGAGCGCTTACCTTCAAGATCTCCCCAAACTGAAC 181

Query: 126 AAACCACTGAGGCCTTGTATTTCAGCTGAGCAGCAAGAATGAAGCCAGTGAATGGTGGCC 185  
AA CCACCTGAGGCCTTGTATTTCAGCTG GCAGCAAG ATGAAGCC G GAATGGTGGCC  
Sbjct: 182 AAGCCACTGAGGCCTTGTATTTCAGCTGGGCAGCAAGGATGAAGCCGGCAGAATGGTGGCC 241

Query: 186 CCGGCTGTCCAGGAGAAGAAGGTGAAAAAGCGGGTGTCTTCGCAGACAACCAGGGGCTG 245  
CC C GT CAGGAGAAGAAGGTGAA AAGCGGGTGTCTTCGC GACAACCAGGGGCTG  
Sbjct: 242 CCCACAGTACAGGAGAAGAAGGTGAAGAAGCGGGTGTCTTCGCCGACAACCAGGGGCTG 301

Query: 246 GCCCTGACAATGGTCAAAGTGTCTCGGAATTCGATGACCCGCTAGATATGCCATTCAAC 305  
GCCCT ACAATGGT AAAGTGTCTCGGAATTCGATGACCC CTAGATAT CC TT AAC  
Sbjct: 302 GCCCTAACAAATGGTGAAGTGTCTCGGAATTCGATGACCCACTAGATATTCCGTTTAAAC 361

Query: 306 ATCACCAGAGCTCTAGACAACATTGTGAGCTTGACGACAGCAGAGAGCGAGAGCTTTGT 365  
ATCAC GAGCTCTAGACAACAT GTGAG TGACGACAGCAGAGAG GAGAGCTTTGT  
Sbjct: 362 ATCACTGAGCTCTTAGACAACATCGTGAGTCTGACGACAGCAGAGAGTGAGAGCTTTGT 421

Query: 366 CTGGATTTTCCAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGGCCGAC 425  
TGGATTTT C CAGCC TCTGCAGATTACTTAGACTTTAGAAATCG CTTCAG CC AC  
Sbjct: 422 TTGGATTTTCCGACCCCTCTGCAGATTACTTAGACTTTAGAAATCGGCTTCAGACCAAC 481

Query: 426 CACGTCTGCCTTGAGAAGTGTGTGCTCAAGGACAAGGCCATTGCAGGCATGTGAAGGT 485  
CA GTCTGCCT GA AACTG GTGCT AAGGA AA GCCAT GC GGCAC GT AAGGT  
Sbjct: 482 CATGTCTGCCTCGAAAACATGCGTGCTGAAGGAGAAAGCCATCGCGGGCACCGTCAAGGTC 541

Query: 486 CAGAACCTCGCATTGAGAAGACCGTGAAAATAAGGATGACGTTTCGACACCTGGAAGAGC 545  
CAGAACCT GCATT GAGAAG GTGAA AT AG ATGAC TTCGA ACCTGGAA AGC  
Sbjct: 542 CAGAACCTGGCATTGAGAAGGTTGTGAAGATCAGCATGACATTTCGATACCTGGAAGAGC 601

Query: 546 TACACAGACTTTCCTTGTGAGTACGTGAAGGACACTTATGCCGGTTTCAGACAGGGACACG 605  
T CACAGACTT CCTTGTGAGTA GTGAAGGACACTTA GC GGTTCAGACAGGGACAC  
Sbjct: 602 TTCACAGACTTCCCTTGTGAGTATGTGAAGGACACTTACGCTGGTTTCAGACAGGGACACA 661

Query: 606 TTCTCCTTCGACATCAGCTTGCCCCGAGAAGATTGAGTCTTATGAAAGAATGGAGTTTGCT 665  
TTCTCCTT GA ATCAGC T CC GAGAA AT CAGTCTTATGAAAGAATGGAGTT GC  
Sbjct: 662 TTCTCCTTGTATATCAGCCTACCGGAGAAAATCCAGTCTTATGAAAGAATGGAGTTTCGCC 721

Query: 666 GTGTACTACGAGTGCAATGGACAGACGTAAGGACAGCAACAGAGGCAAGAACTATAGG 725  
GTGT CTACGAGTG AA GG CAG CGTACTGGGACAGCAACA AGGCAA AACTA AGG  
Sbjct: 722 GTGTACTACGAGTGTAACGGCCAGTCGTACTGGGACAGCAACAAAGGCAAAACTACAGG 781

Query: 726 ATCATCCGGGCTGAGTTAAAATCTACCCAGGGAATGACCAAGCCCCACAGTGGACCGGAT 785  
ATCA C GGGC GA T A ATC ACCCAGGGAATGAC AGCC ACA TGG CCGGAT  
Sbjct: 782 ATCACCAGGGCCGAACCTCAGATCCACCCAGGGAATGACTGAGCCGTACAATGGGCCGGAT 841

Query: 786 TTGGGAATATCCTTTGACCAGTTTCGGAAGCCCTCGGTGTTCTTATGGTCTGTTTCCAGAG 845  
TT GGAAT TC TTTGACCAGTTTCGG AGCCCTCGGTGTTCTT GG CTGTTTCCAGAG  
Sbjct: 842 TTTGGAATCTCTTTTACCAGTTTCGGGAGCCCTCGGTGTTCTTTCGCCCTGTTTCCAGAG 901

Query: 846 TGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTACTAGTGA-----CTGCAGG 900  
TGGCC AGTTA T GG TATGAAAAGCT GGGCCCTA TACTAGTGA CTGCAG  
Sbjct: 902 TGGCCTAGTTATCTGGGGTATGAAAAGCTGGGGCCCTATTACTAGTGAAGTTGACTGCAGT 961

Query: 901 TGACAG 906  
TGACAG  
Sbjct: 962 TGACAG 967

FIG. 29

Score = 1366 (480.9 bits), Expect = 1.3e-139, P = 1.3e-139  
Identities = 255/284 (89%), Positives = 270/284 (95%)

Query: 2 MAVDIEYRYNCMAPSLRQERFAFKISPKPSKPLRPCIQLSSKNEASGMVAPAVQEKVKK 61  
MAVDIEY Y+ MAPSLR+ERF FKISPK +KPLRPCIQL SK+EA MVAP VQEKVKK  
Sbjct: 1 MAVDIEYSYSSMAPSLRRERFTFKISPKLNKPLRPCIQLGSKDEAGRMVAPTQEKVKK 60

Query: 62 RVSFADNQGLALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESESFVLDFSQPSADY 121  
RVSFADNQGLALTMVKVFSEFDDPLD+PFNITELLDNIVSLTTAESESFVLDF QPSADY  
Sbjct: 61 RVSFADNQGLALTMVKVFSEFDDPLDIPFNITELLDNIVSLTTAESESFVLDFPQPSADY 120

Query: 122 LDFRNRLQADHVCLENCVLKDKAIAAGTVKVQNLAFEKTVKIRMTFDTWKS YTDFFPCQYVK 181  
LDFRNRLQ +HVCLENCVLK+KAIAGTVKVQNLAFEK VKIRMTFDTWKS+TDFPCQYVK  
Sbjct: 121 LDFRNRLQTNHVCLENCVLKEKAIAGTVKVQNLAFEKVVKIRMTFDTWKSFTDFPCQYVK 180

Query: 182 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVYYECNGQTYWDSNRGKNYRIIRAELKSTQ 241  
DTYAGSDRDTFSFDISLPEKIQSYERMEFAV YECNGQ+YWDSN+GKNYRI RAEL+STQ  
Sbjct: 181 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVCYECNGQSYWDSNKGKNYRITRAELRSTQ 240

Query: 242 GMTKPHSGPDLGISFDQFGSPRCSYGLFPEWPSYLGYEKLGPPY 285  
GMT+P++GPD GISFDQFGSPRCS+GLFPEWPSYLGYEKLGPPY  
Sbjct: 241 GMTEPYNGPDFGISFDQFGSPRCSFGLFPEWPSYLGYEKLGPPY 284

FIG. 30

Based on this alignment, black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties); greyed amino acid residues can be mutated to a residue with comparable steric and/or chemical properties without altering protein structure or function (e.g. L to V, I, or M); non-highlighted amino acid residues can potentially be mutated to a much broader extent without altering structure or function.

```

Q63759_PP1_RAT      -----MAVDIEYSYSSMAPSLR--RERFTFKISPKLNKPLRPCIQLG
AC016485_A          -----MMAVDIEYRYNCMAPSLR--QERFAFKISPKPSKPLRPCIQLS
O08541_PP1_MOUSE    -----MAMRICLAHSPPPLKSFLLGPNYNGFQRRNFVNKLKPLKPLSV-
AAD33215_PPP1R5_HUMAN MIQVLDPRPLTSSVMPVDMAVRECLAHSPPVKSFLLGPNYDEFQRRHFVNKLKPLKSCINI-

Q63759_PP1_RAT      SKDEAGRMVAPTVQEKKVKKRVSFADNQGLALTMVKVFSEFDDP--LDIPFNITELLNDI
AC016485_A          SKDEAGSMVAPAVQEKKVKKRVSFADNQGLALTMVKVFSEFDDP--LDMPFNITELLNDI
O08541_PP1_MOUSE    -KQEAKSQSEWKSPPHNQAKKRVVFADSKGLSLTAIHVFSDLPEEPAWDLQFDLLDLNDIS
AAD33215_PPP1R5_HUMAN -KHKAQSQNDWKCASHNQA KKRNVVFADSKGLSLTAIHVFSDLPEEPAWDLQFDLLDLNDIS

Q63759_PP1_RAT      VSLTTAESESFVLDFPQP SADYLD FRNRLQTNHVCLENCVLKEKAIACTVKVQNLAFEKV
AC016485_A          VSLTTAESESFVLDFSPQ SADYLD FRNRLQADHVCLENCVLKDKAIACTVKVQNLAFEKT
O08541_PP1_MOUSE    SSLKLHEEKNLWFDFFPQPSTDYLSFRDRFQKNFVCLENCSLDRTVTCTVKVKNVSEFEKK
AAD33215_PPP1R5_HUMAN SALKHHEEKNLWLDFFPQPSTDYLSFRSHFQKNFVCLENCSLQERTVTCTVKVKNVSEFEKK

Q63759_PP1_RAT      VKIRMTFDTWKSETDFPCQYVVKDTYAGSDRDTFSFDISLPEKIQSYERMEFAVCYECNGQ
AC016485_A          VKIRMTFDTWKS YTD FPCQYVVKDTYAGSDRDTFSFDISLPEKIQSYERMEFAVYYECNGQ
O08541_PP1_MOUSE    VQVRITFDTWK YTDVD CVYMKNVYS SSSDSDTFSFAIDLPRVIPTEEKIEFCISYHANGR
AAD33215_PPP1R5_HUMAN VQIRITFDSWK NYTDVD CVYMKNVYSGGSDSDTFSFAIDLPPVIPTEQKIEFCISYHANGQ

Q63759_PP1_RAT      SYWDSNKGKNYRITRAELR--STQGMTEPYN-----GPDFGISFDQFGSPRCSFGLFPE
AC016485_A          TYWDSNKGKNYRITRAELK--STQGMTKPHS-----GPDLGISFDQFGSPRCSYGLFPE
O08541_PP1_MOUSE    IFWDNNEGQNYRIVHVQWKPDGVQTQVAPKDCAFOGPPKTEIEPTVFGSPRLASGLFPE
AAD33215_PPP1R5_HUMAN VFWDNNDGQNYRIVHVQWKPDGVQTQMAPQDCARHOTS PKTEIEESTIFGSPRLASGLFPE

Q63759_PP1_RAT      WPSYLGYEKLGPYY
AC016485_A          WPSYLGYEKLGPYY
O08541_PP1_MOUSE    WQSWGRVENLTSYR
AAD33215_PPP1R5_HUMAN WQSWGRMENLASYR

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**FIG. 31**

CTGTCTCCTGCATTCTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGC  
TACTACCGCTTTGTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATC  
AGCTTGGCTGTGCGGAAGATCGCGCTGCTGCTGAAGCCGGACAAGGAGATCGAACA  
CCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTTCCGAAACTACACTGTGC  
AGTTTGATGTGGGAGTGGAGTTTGAGGAGGACCTCAGGAGCGTGGACGGACGAAAA  
TGCCAGATCTCATTCGTCGGTTCGGATCCAAGCCAGTTCTGTGGTCAGCAAGGCTCC  
CCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGTTTGCGG  
CTGACCTTCCGCACACAGCCTTCCTCGGAGAACAAGACTGCCCCACCTCCACAAGGGC  
TTCCTGGCCCTCTACCAAACCGTGGCCTTAAGTGGAAGCTTGAGTGACAGCTGAGGC  
TGGGGACTCAGGGACACCTGGGCTGGATCCCAGCCCTGCC

**FIG. 32**

MPPNLTGYRFSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFR  
NYTVQFDVGVEFEEDLRSVDGRKCQISFVGSDPSQFCGQQGSPLGRPPGQREFVSSGRSL  
RLTFRTQPSSSENKTAHLHKGFLALYQTVALSGSLSDS

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

FIG. 33

Score = 355 (125.0 bits), Expect = 1.0e-31, P = 1.0e-31  
Identities = 68/70 (97%), Positives = 70/70 (100%), Frame = +2

Query: 38 MPPNLTGYRFSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 217  
MPPNLTGYRFSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN  
Sbjct: 1 MPPNLTGYRFSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 60

Query: 218 YTVQFDVGVE 247  
YT+QFDVGV+  
Sbjct: 61 YTLQFDVGVQ 70

**FIG. 34**

CTGTCTCCTGCATTCTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGCTACTACCGCTTT  
GTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATCAGCTTGGCTGTGCGGAAGATCGCGC  
TGCTGCTGAAGCCGGACAAGGAGATCGAACACCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTT  
CCGAAACTACACTGTGCAGTTTGATGTGGGAGTGGAGTTTGAGGAGGACCTCAGGAGCGTGGACGGACGA  
AAATGCCAGACCATAGTAACCTGGGAGGAGGAGCACCTGGTGTGTGTGCAGAAAGGGGAGGTCCCCAACC  
GGGGCTGGAGACACTGGCTGGAGGGAGAGTTGCTGTATCTGGAAGTGAAGGATGCAGTGTGCGA  
GCAGGTCTTCAGGAAGGTCAGATAGCCGGAGAGGAGCCAAGATCCCTCCAGACAGCACCAGCTCACAGAC  
GCTCTTGTTGTGCCCCCTTCAAGCCCAGATTGTGCCAGATCTCATTCGTCGGTTCGGATCCAAGCCAGTT  
CTGTGGTCAGCAAGGCTCCCCCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGT  
TTGCGGCTGACCTTCCGCACACAGCCTTCCTCGGAGAACAAGACTGCCACCTCCACAAGGGCTTCCTGG  
CCCTCTACCAAACCGTGGGTGAGTGTCCCTCCTGGGGCTGCAGGGAGGGAGCCTCTGTTCCAGCCATGA  
CCCTGGTATCTTCAAGCCTTAAGTGGAAGCTTGAGTGACAGCTGAGG

**FIG. 35**

MPPNLTGYRFRVFSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRNYTVQFDVGVE  
FEEDLRSVDGRKCQTIVTWEEHLCVQKGEV PNRGWRHWLEGELLYLELTARDAVCEQVFRKVR

FIG. 36

Score = 712 (250.6 bits), Expect = 1.5e-69, P = 1.5e-69  
Identities = 133/135 (98%), Positives = 135/135 (100%), Frame =  
+2

Query: 38 MPPNLTGYRFFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 217  
MPPNLTGYRFFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN  
Sbjct: 1 MPPNLTGYRFFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRN 60

Query: 218 YTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPSNRGWRHWLEGE+LYLEL 397  
YT+QFDVGVEFEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPSNRGWRHWLEGE+LYLEL  
Sbjct: 61 YTLQFDVGVEFEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPSNRGWRHWLEGE+LYLEL 120

Query: 398 TARDAVCEQVFRKVR 442  
TARDAVCEQVFRKVR  
Sbjct: 121 TARDAVCEQVFRKVR 135

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[illegible]